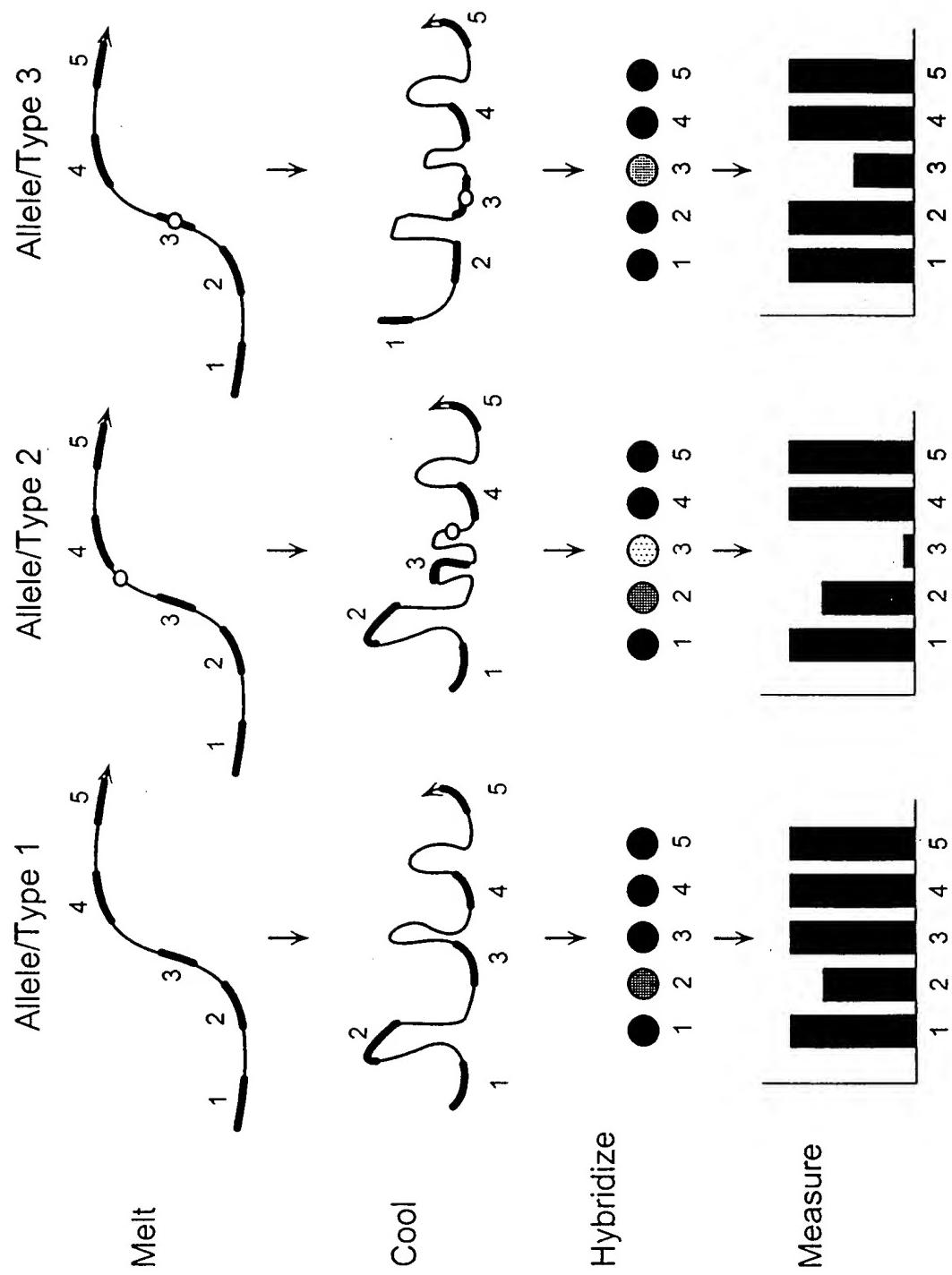


FIGURE 1



BEST AVAILABLE COPY

FIGURE 2

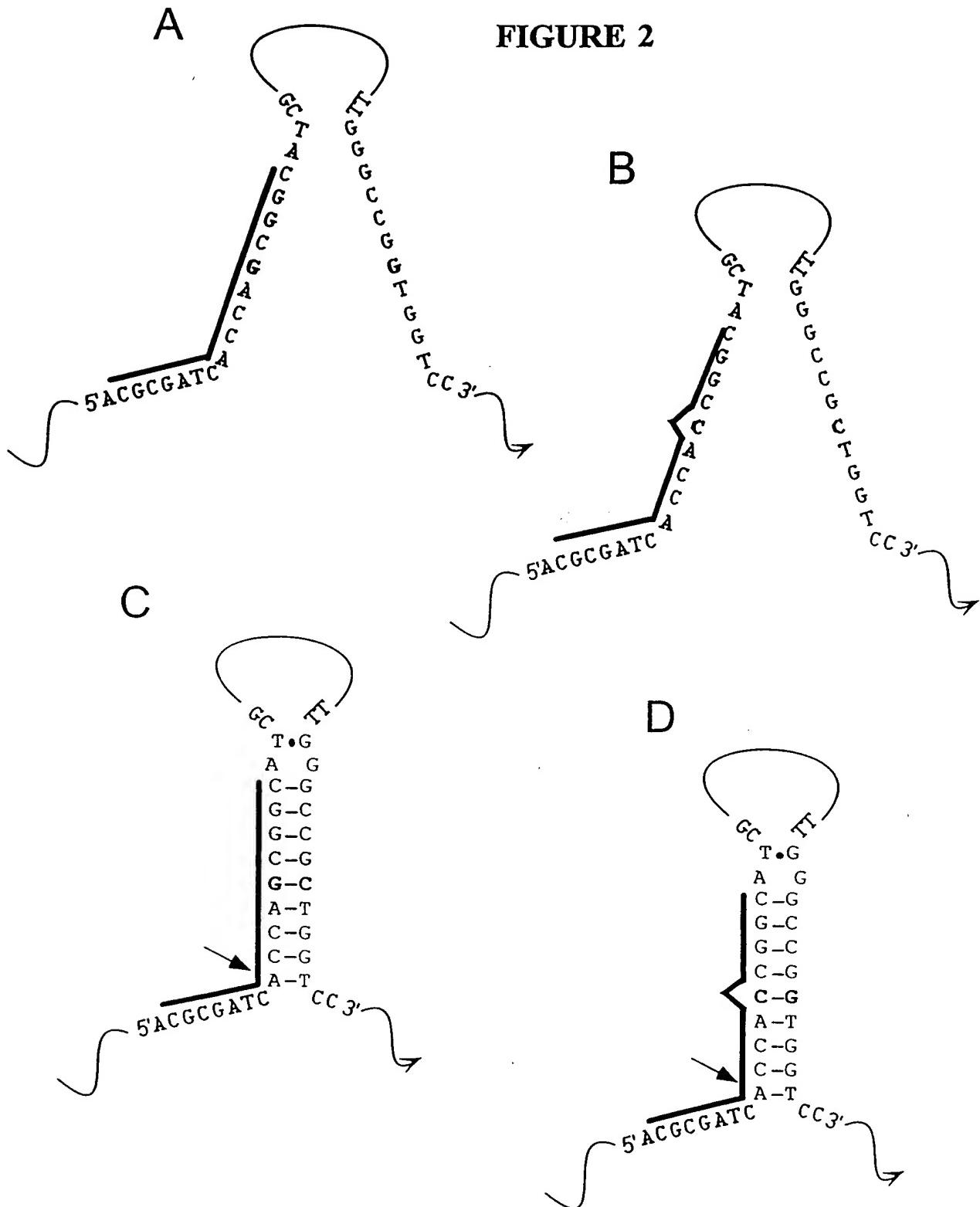


FIGURE 3

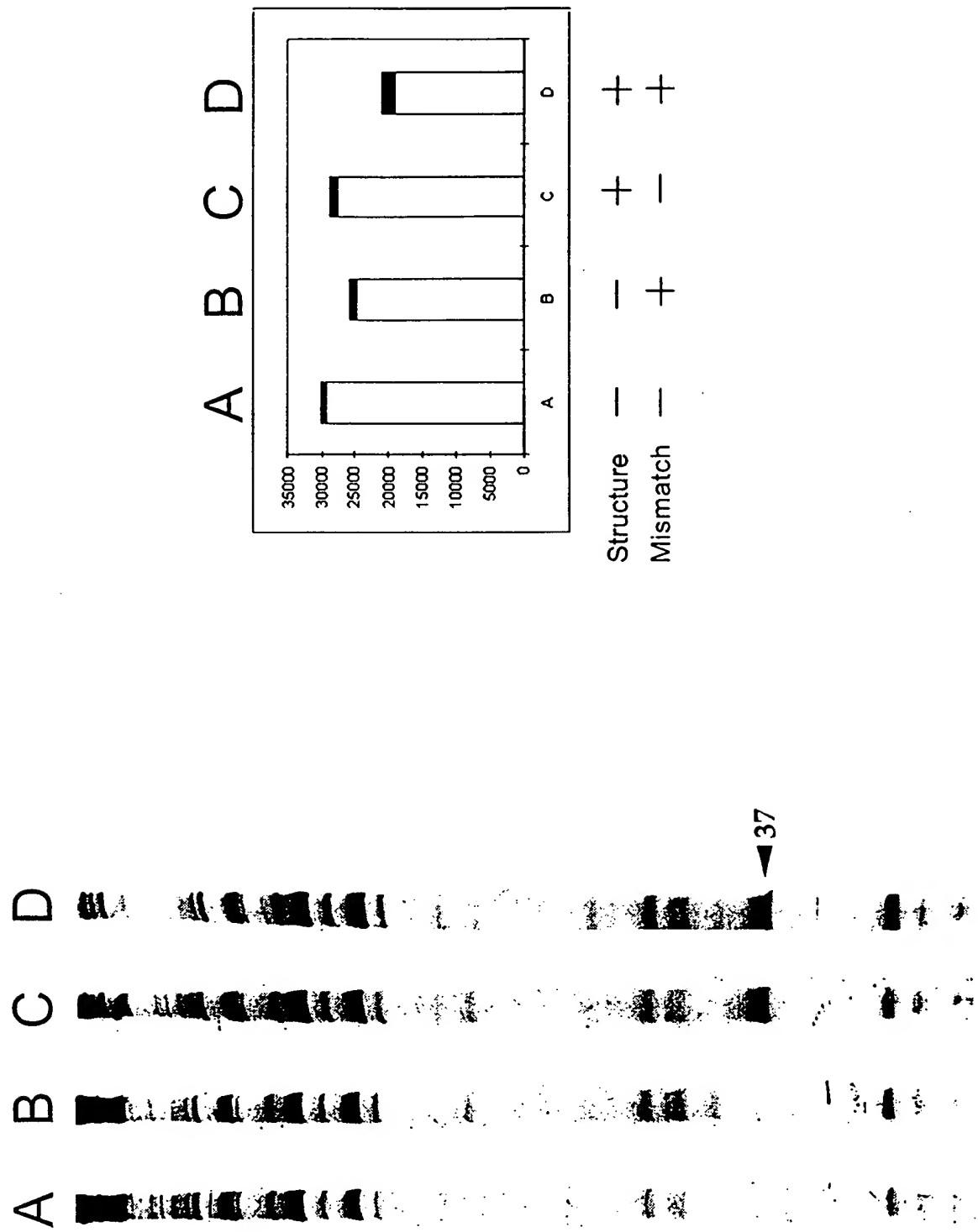


FIGURE 4

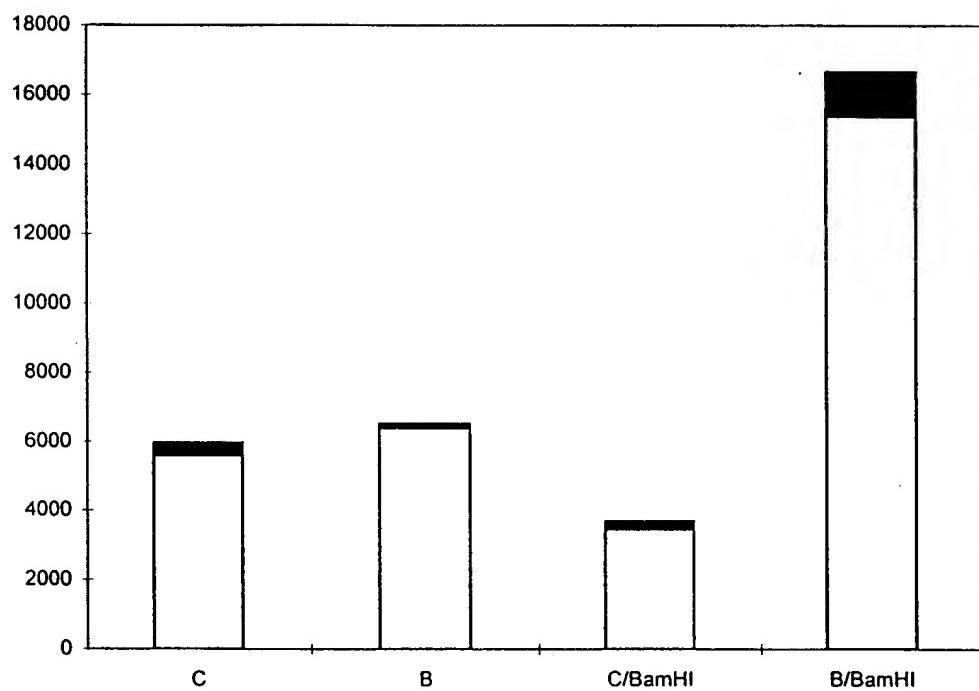


FIGURE 5

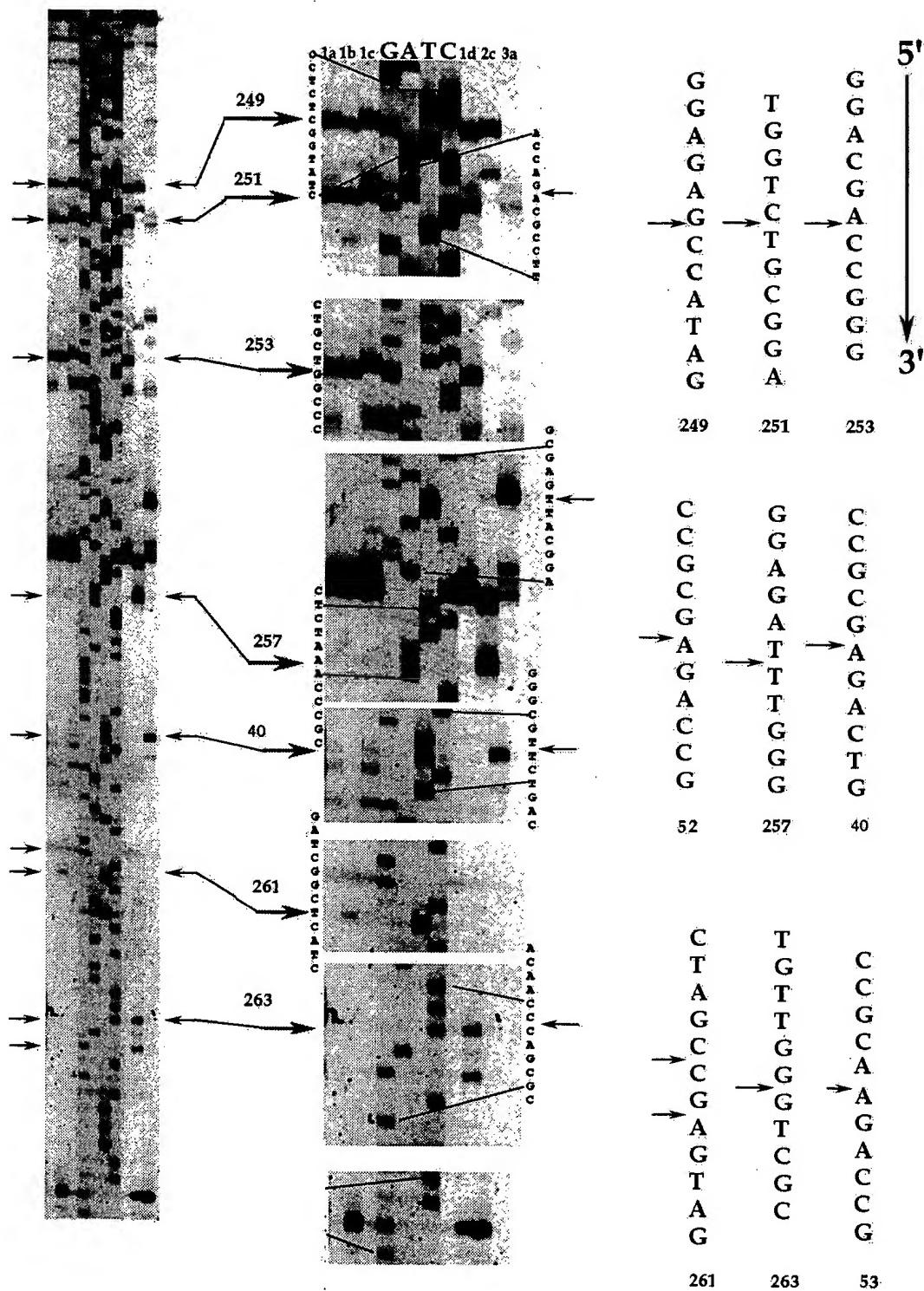


FIGURE 6

Consensus: GATTCTGTCT TCACGGAGAA AGCGTCTAGC CATGGCGTTA GTATGAGTGT CGTGCGAGCCT

HCV 1a -----
HCV 1b -----
HCV 2c -----
HCV 3a ----- C-----

#249 CCAGGACCCC CCCTCCGGGG AGAGGCCATAG TGGTCTTGCGGG AACCGGTGAG TACACCGGAA

-----T-----
-----C-----
-----A-----

#251 #253 TTGCAGGGAC GACCGGGTCC TTTCTTGGAT CAACCCGGTC AATGCCCTGGAA GATTTGGGCC

-----G---A---T----- A---A--- T---C---C C---
-C---TG---GT----- G----- A---CA--- A---

#257 #261 #40 #263 TGCCCCGGCA AGACTGCTAG CCGAGTAGTG TGGGGTCGGG AAAGGCCCTTG TGGTACTGCC

-----G-----
-----C---
-----G---TCA-----

TGATAGGGTG CTTGGGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCAATC

-----A-----

FIGURE 7

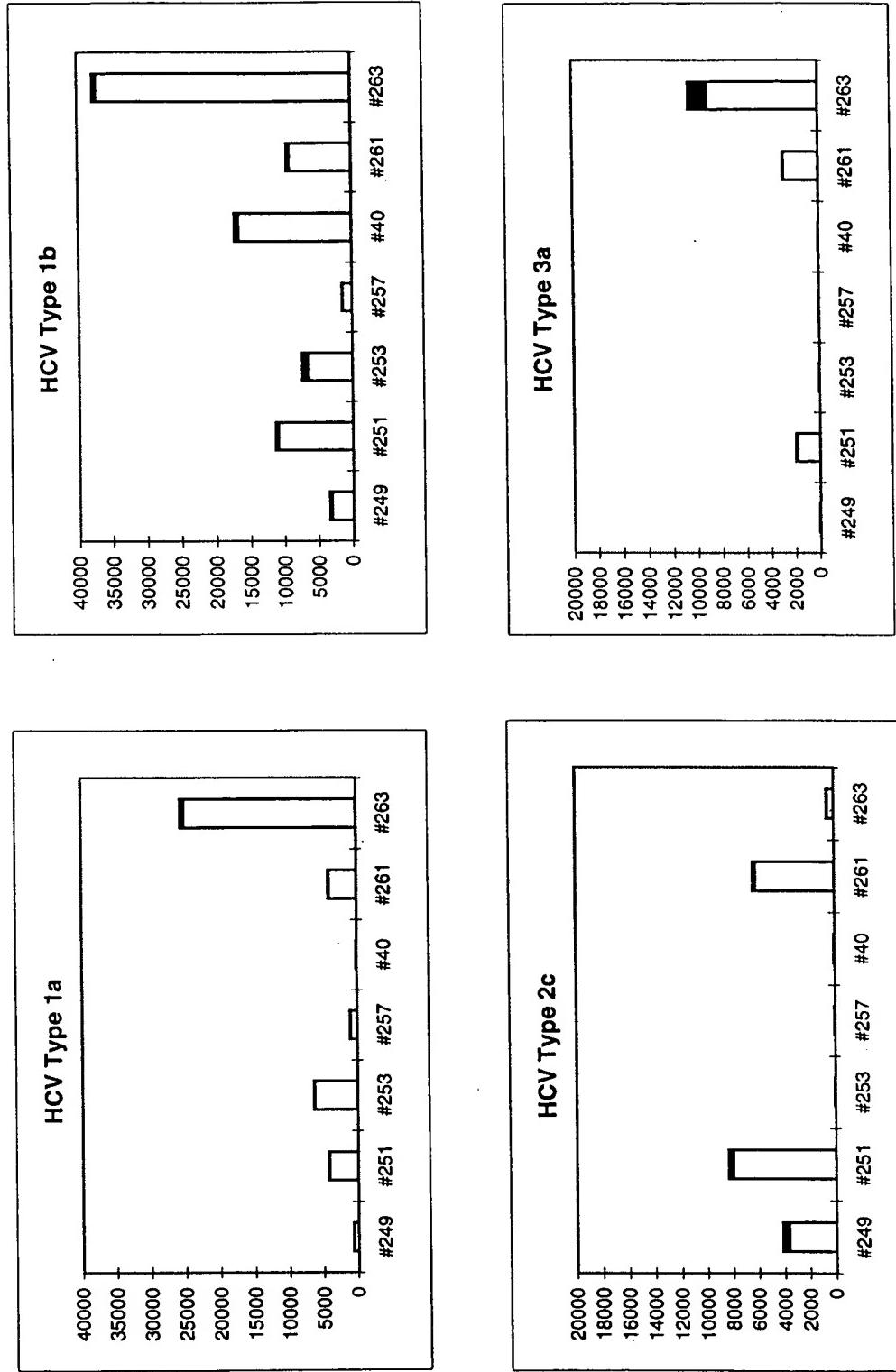


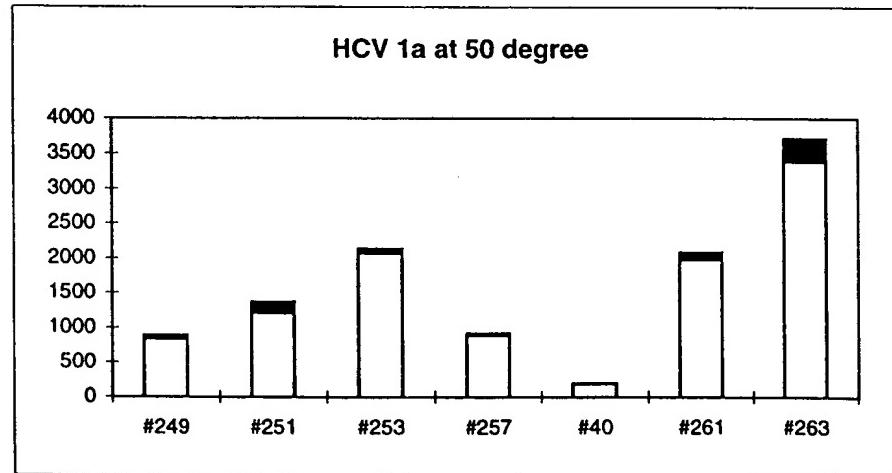
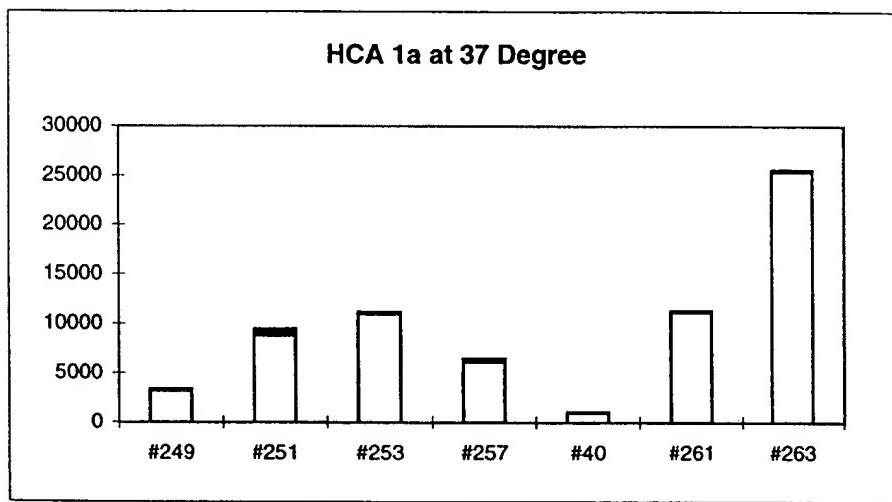
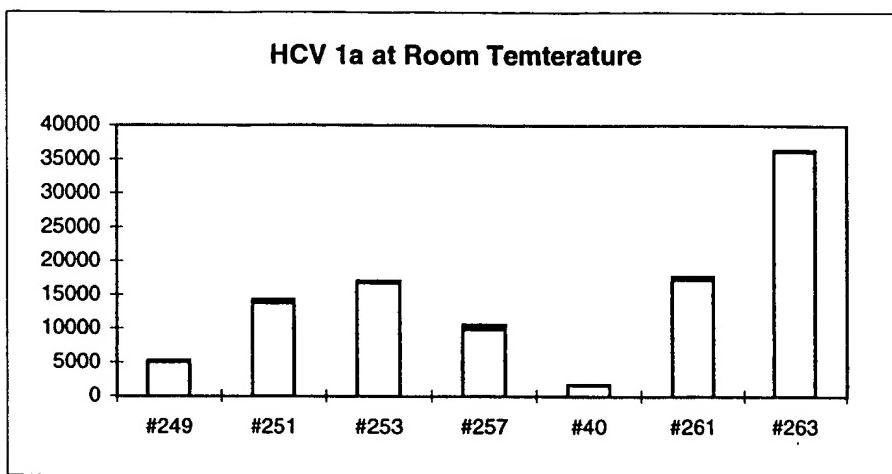
FIGURE 8A

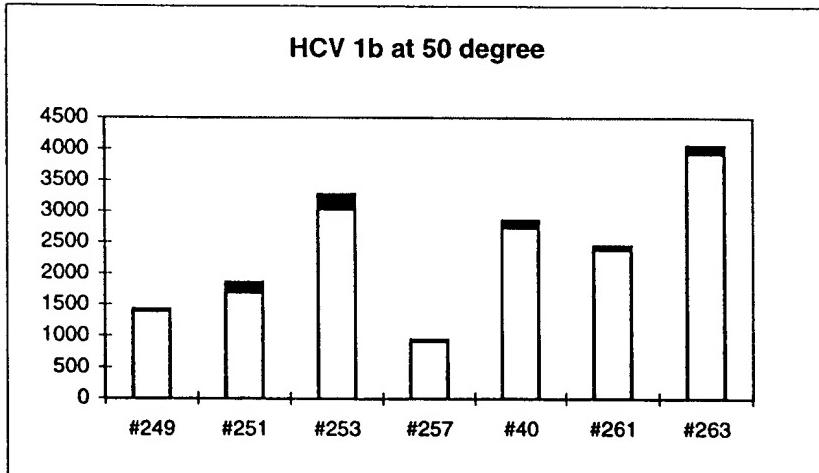
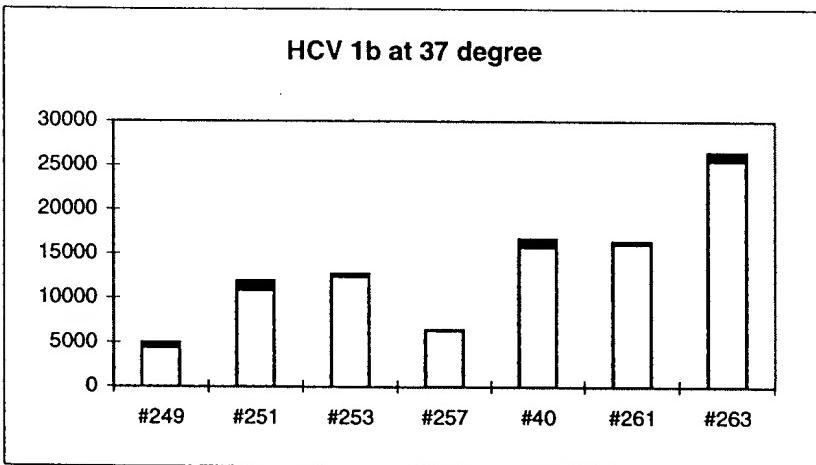
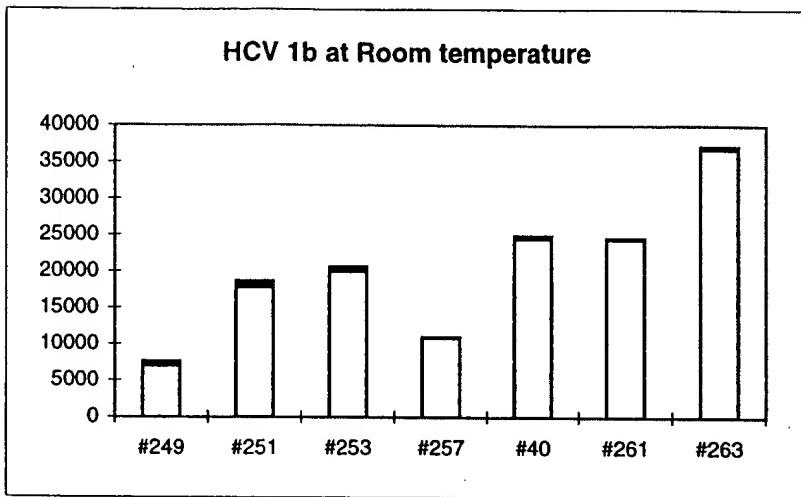
FIGURE 8B

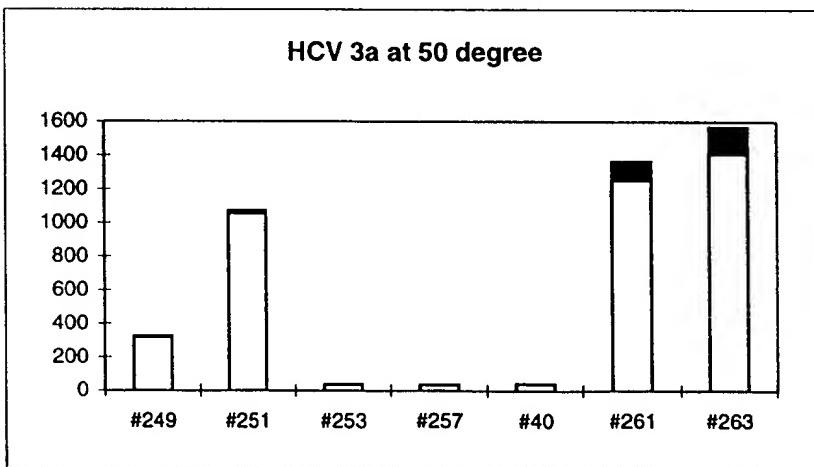
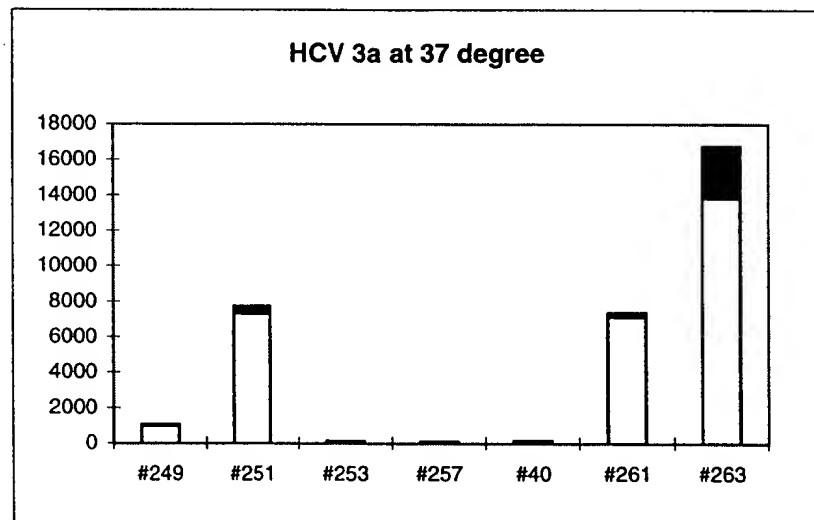
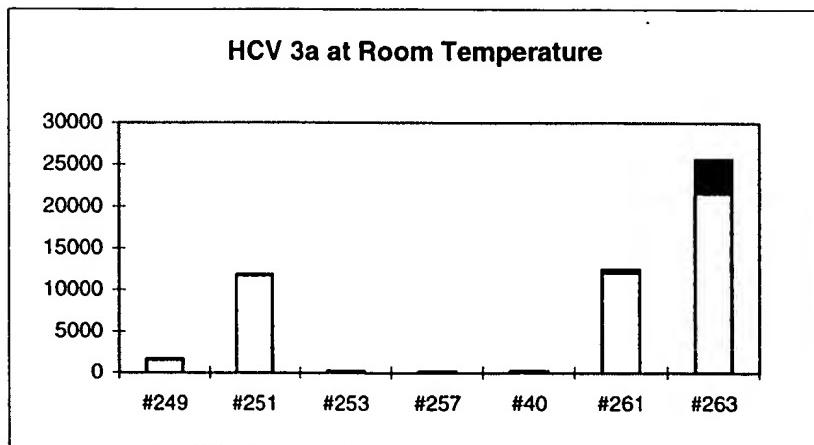
FIGURE 8C

FIGURE 9A

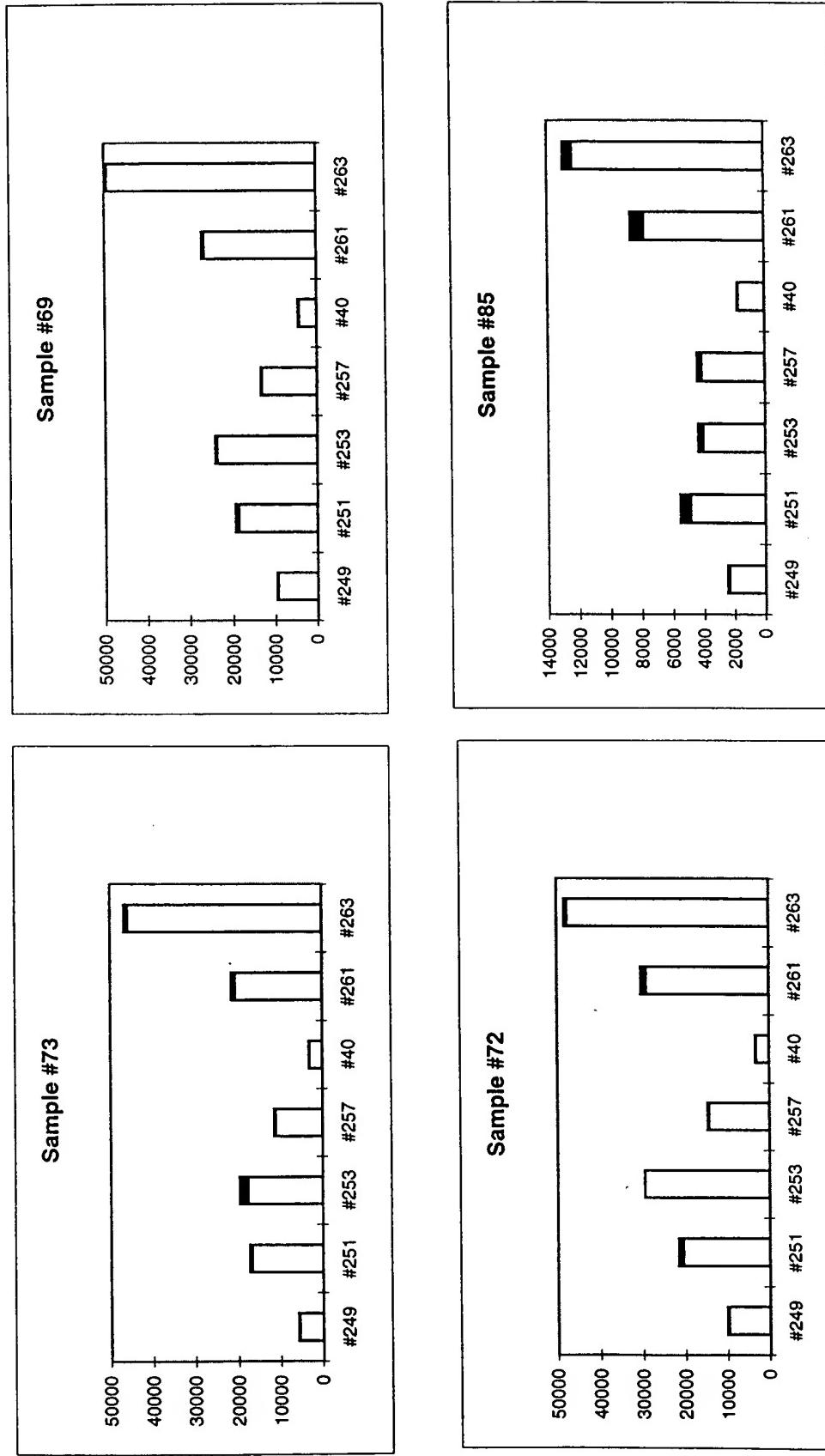


FIGURE 9B

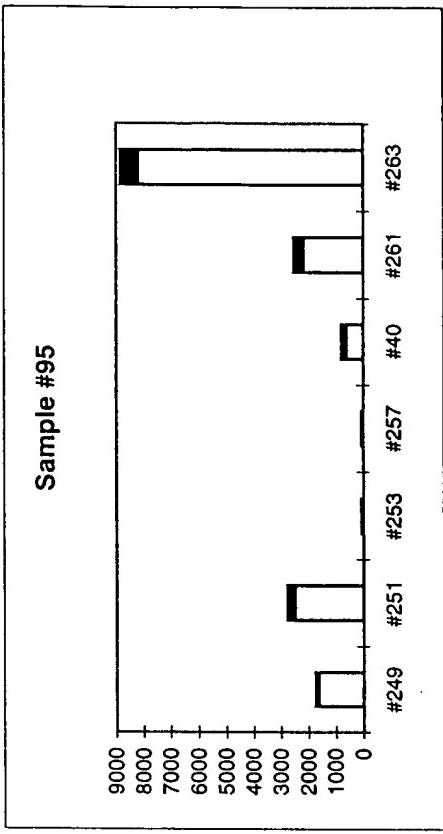
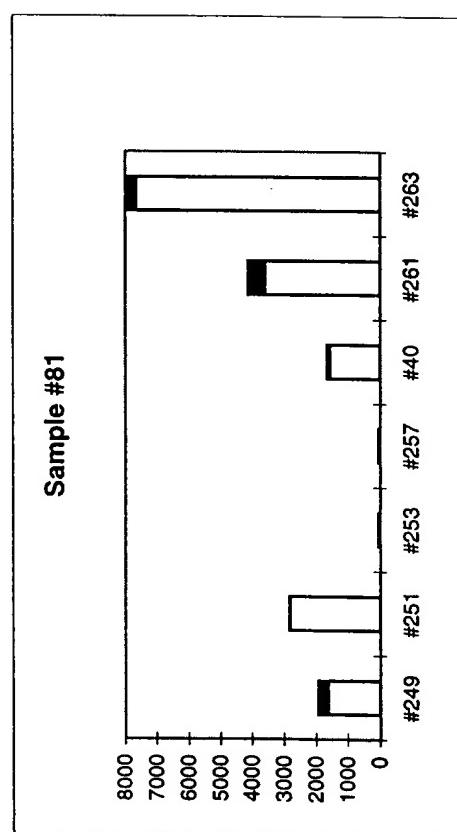
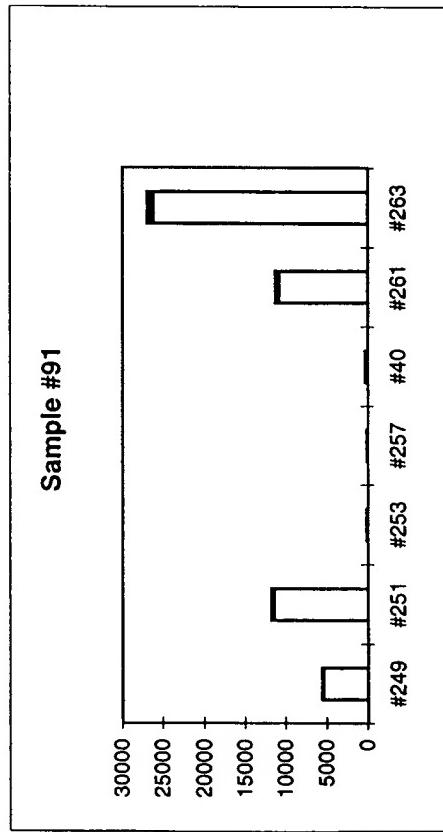


FIGURE 9C

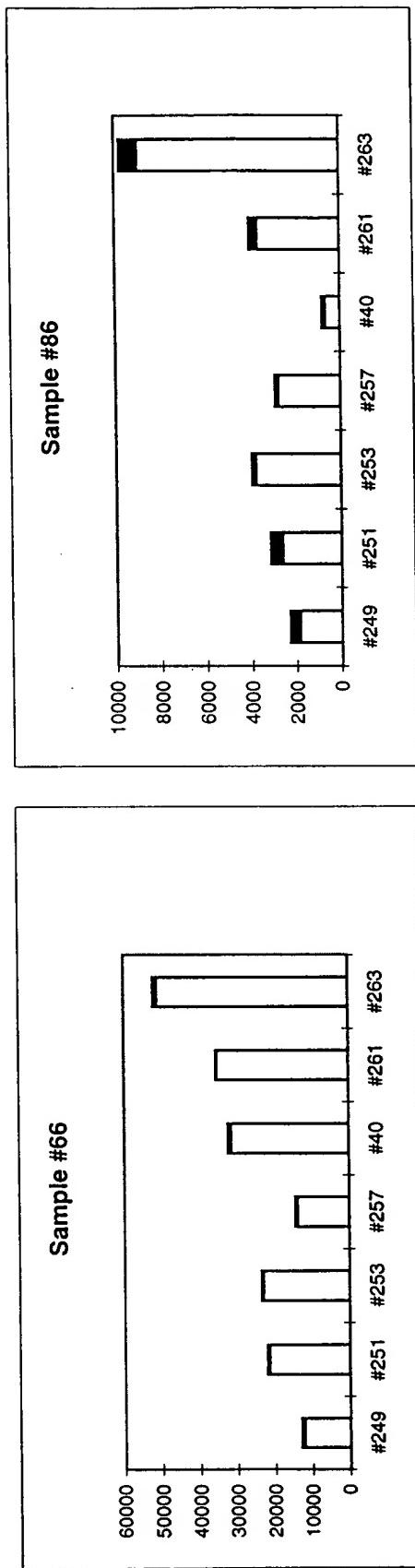


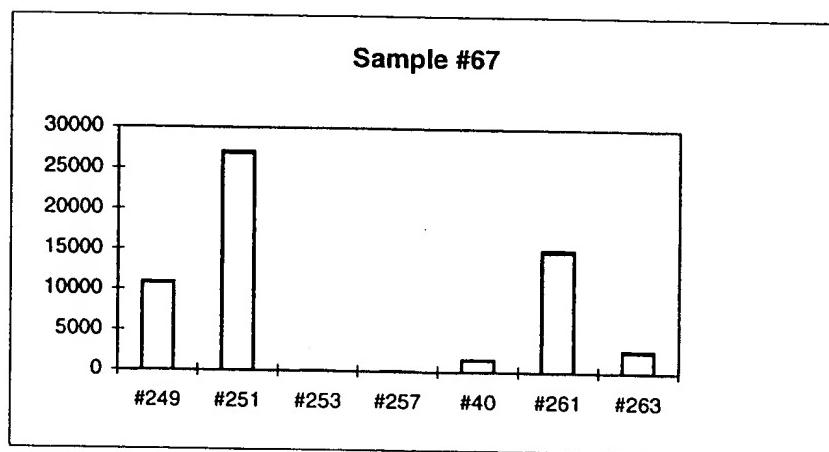
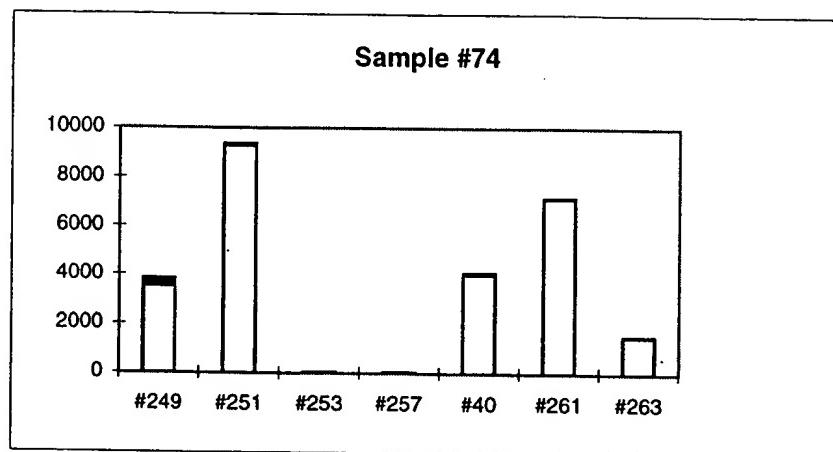
FIGURE 9D

FIGURE 10

#80

A
G A
T — A
C — G
T — A
G — C
T — A
C — G
G — C
C — G

5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

#81

A
G A
T — A
C — G
T — A
G — C
T T
C C
G — C
C — G

5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

#82

G A A
T T
C T T
T T T
G T T
T C T
G T
C T
G T
C T

5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

FIGURE 11A

#2) 5' Biotin

```

      |
      T   A
      C   G   A
      A   T — A
      G   C — G
      A   T — A
      C   G — C
      A   T — A
      G   C — G
      C   G — C
      G   C — G
  
```

#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

#FD91) 3' Biotin - C G A G A G A C C A - 5'

```

          A
          G   A
          T — A
          C — G
          T — A
          G — C
          T — A
          C — G
          G — C
          C — G
  
```

#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

#78) 3' - A G A C C A T T A C C A G A -Biotin 5'

#4) 3' - G A G A C C A T T A C C A G A G -Biotin 5'

#79) 3' - A G A G A C C A T T A C C A G A G A -Biotin 5'



#116) 3' - A G A G A C C A A C C A G A G A -Biotin 5'

#117) 3' - T A C C A G A G A -Biotin 5'

#118) 3' - A G A G A C C A T - 5'

FIGURE 11B

A
 G A
 T — A
 C — G
 T — A
 G — C
 T — A
 C — G
 G — C
 C — G
 #80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'
 #79) 3' - A G A G A C C A — T T — A C C A G A G A -Biotin 5'

A

G	A
T	— A
C	— G
T	— A
G	— C
T	— A
C	— G
G	— C
C	— G

#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

3' - A G A G A C C A A C C A G A G A -Biotin 5'

	T	T
#115	T	T
	A	A
	C	C
A	↔ C	C
	A	↔ A
	G	
C	↔ A	A
	G	G
A		A

Biotin 5' 3'

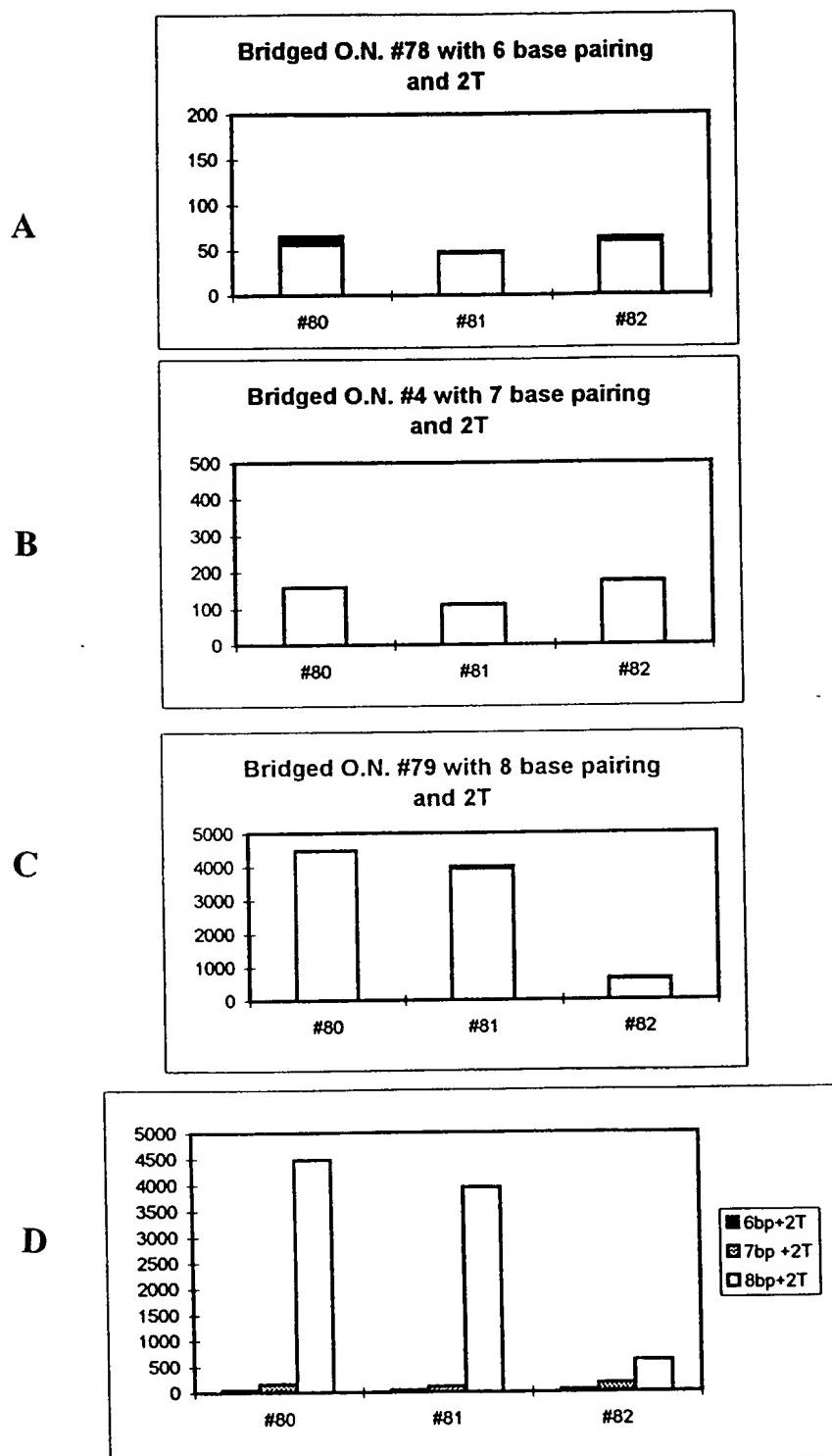
FIGURE 12

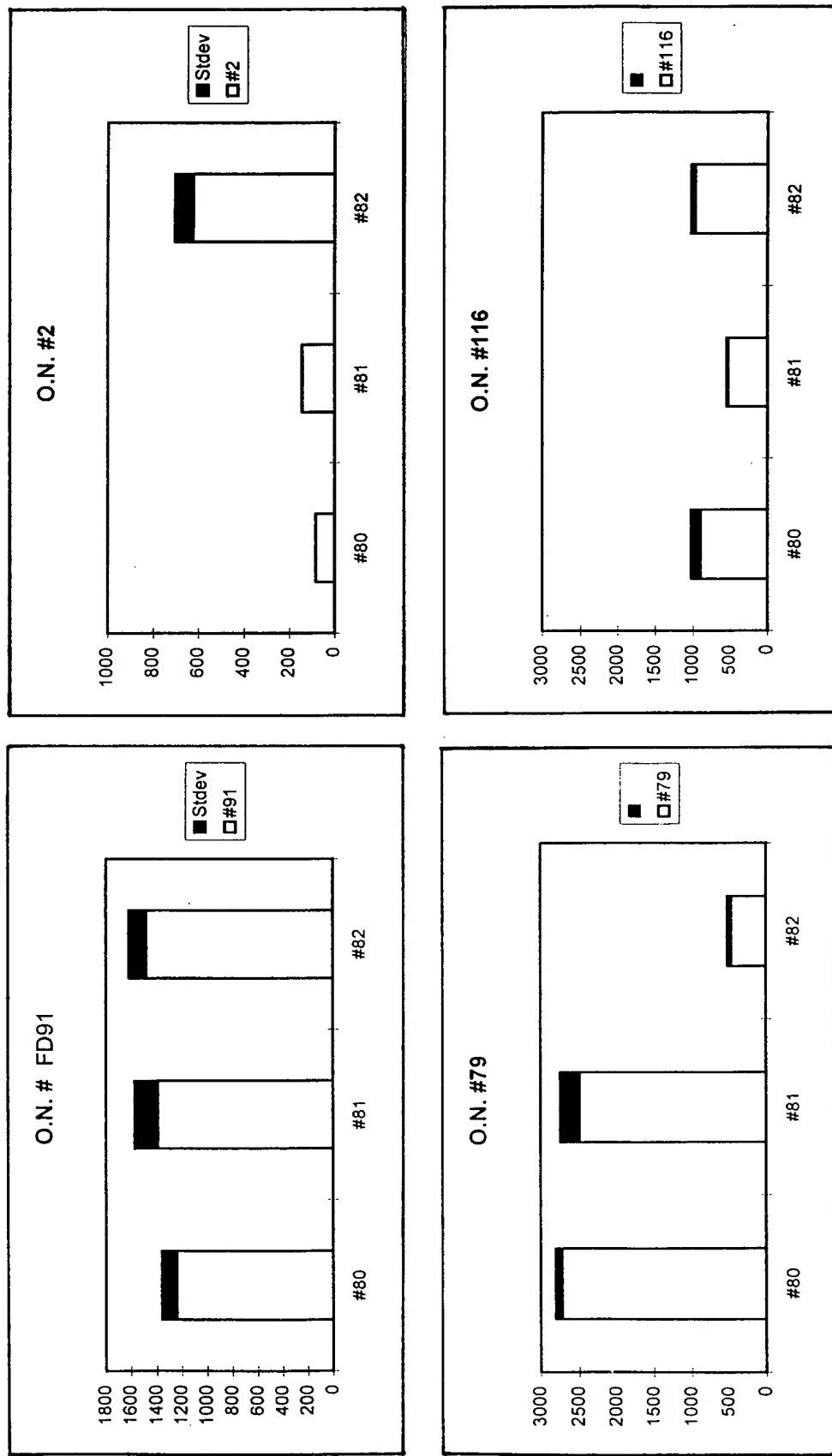
FIGURE 13A

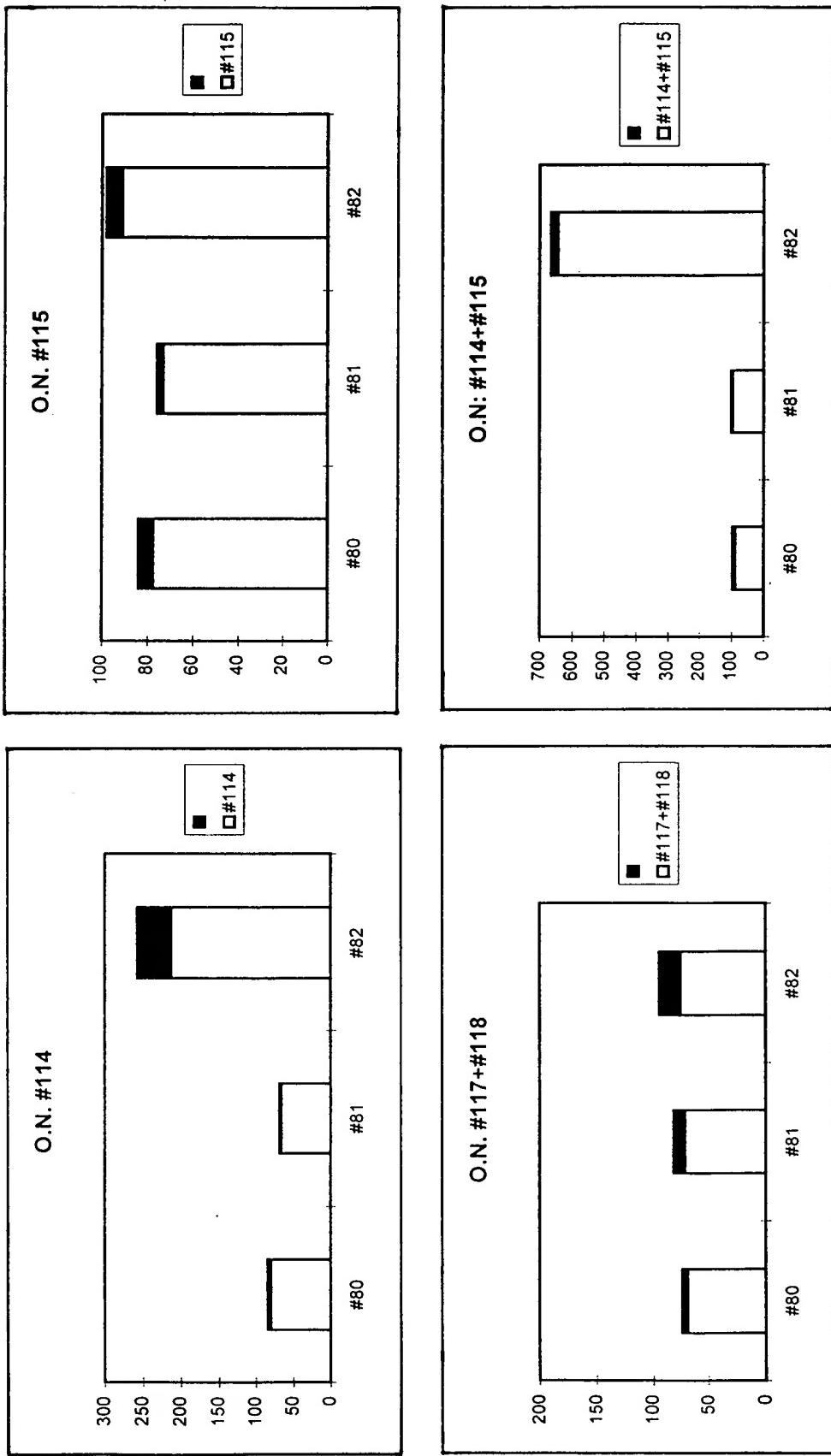
FIGURE 13B

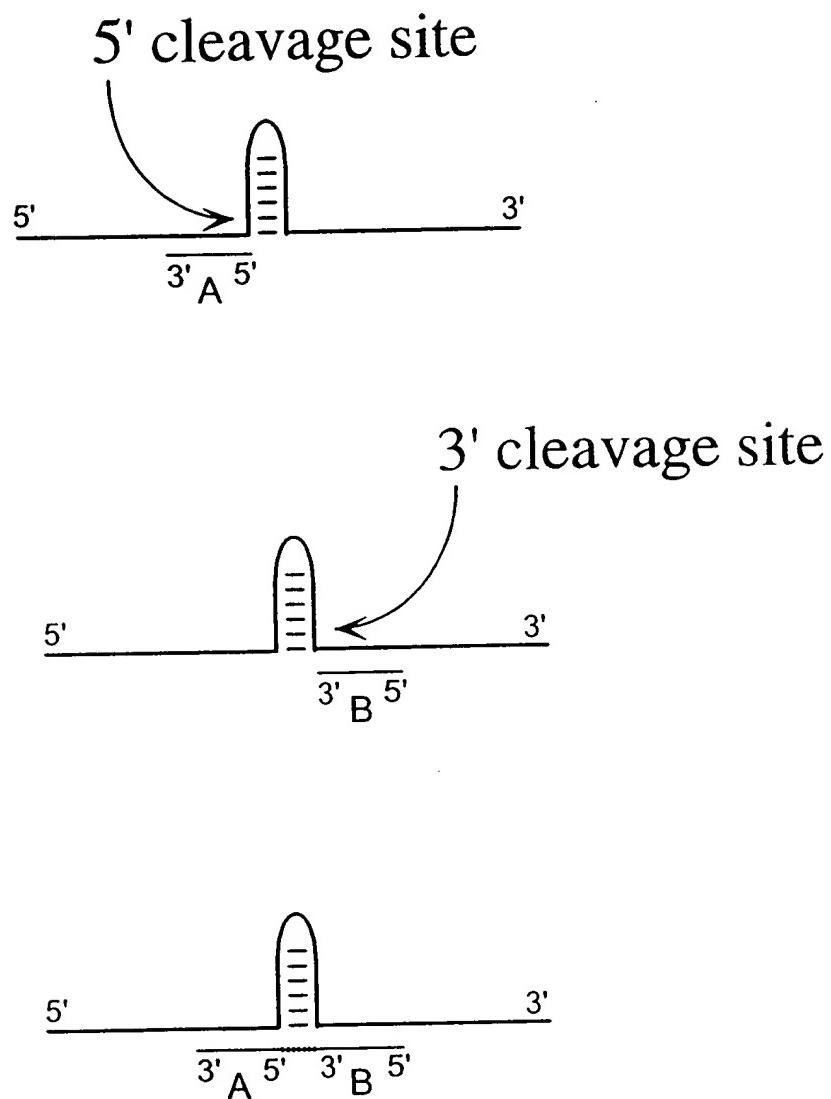
FIGURE 14

FIGURE 15

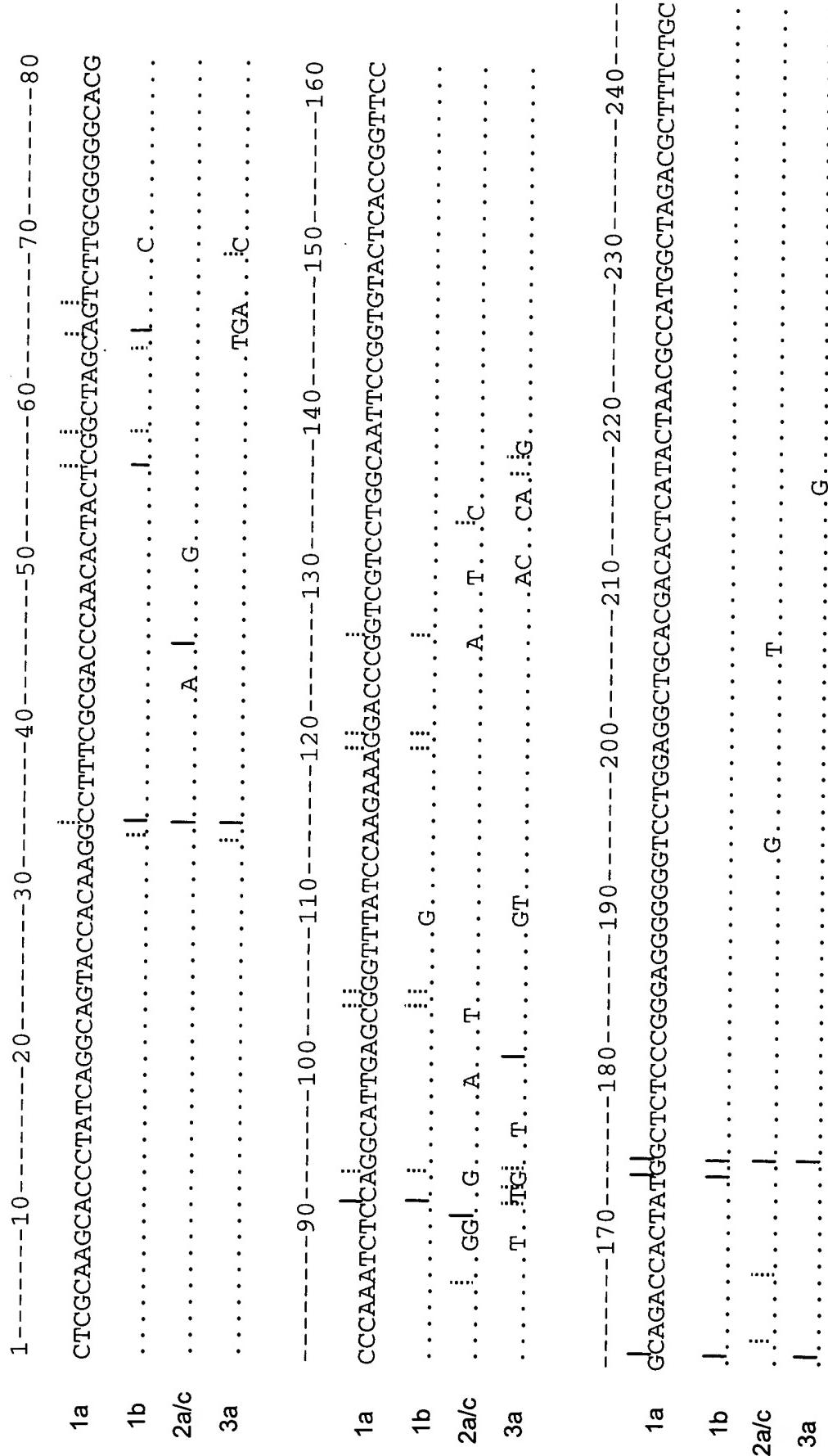


FIGURE 16A

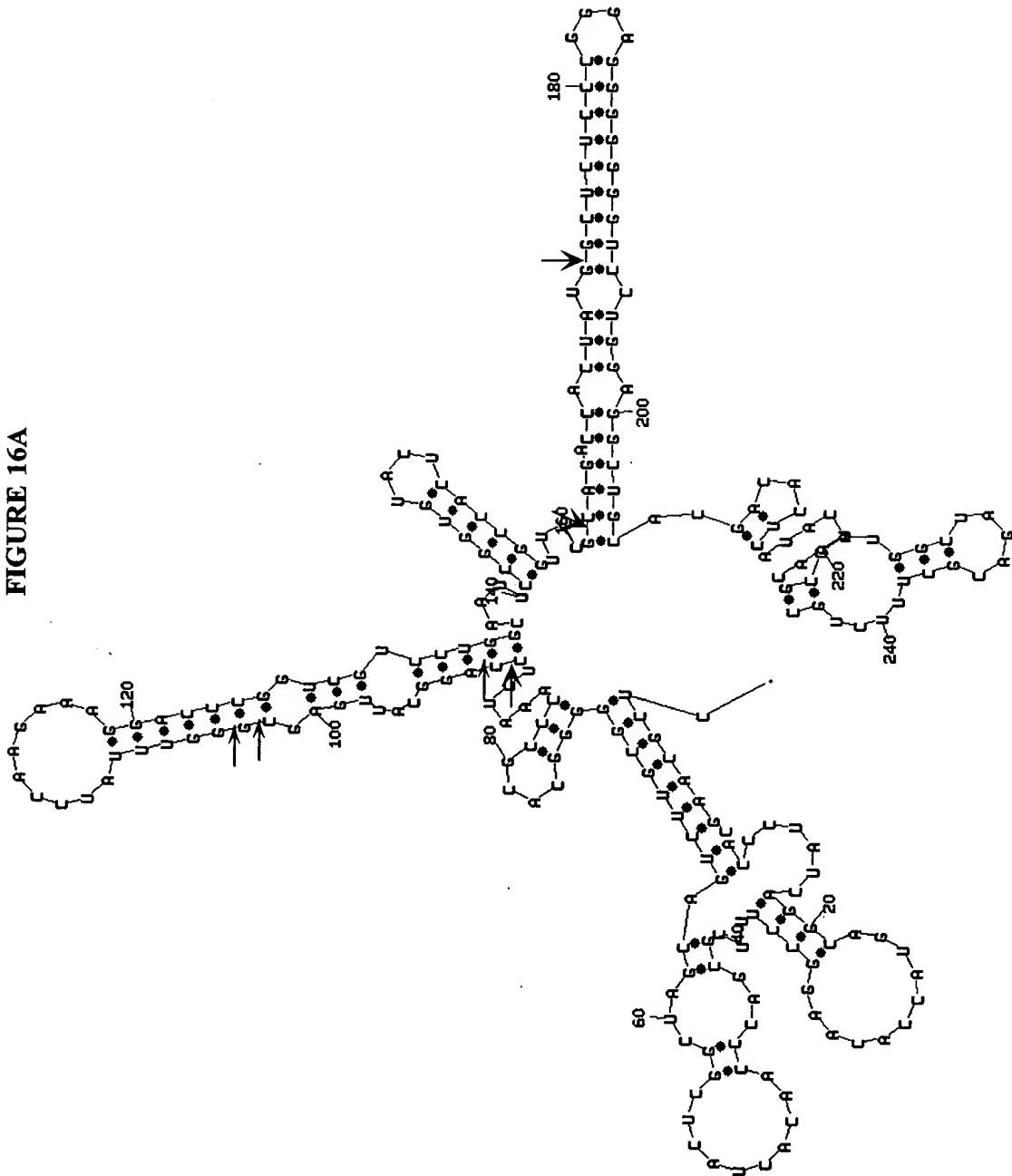


FIGURE 16B

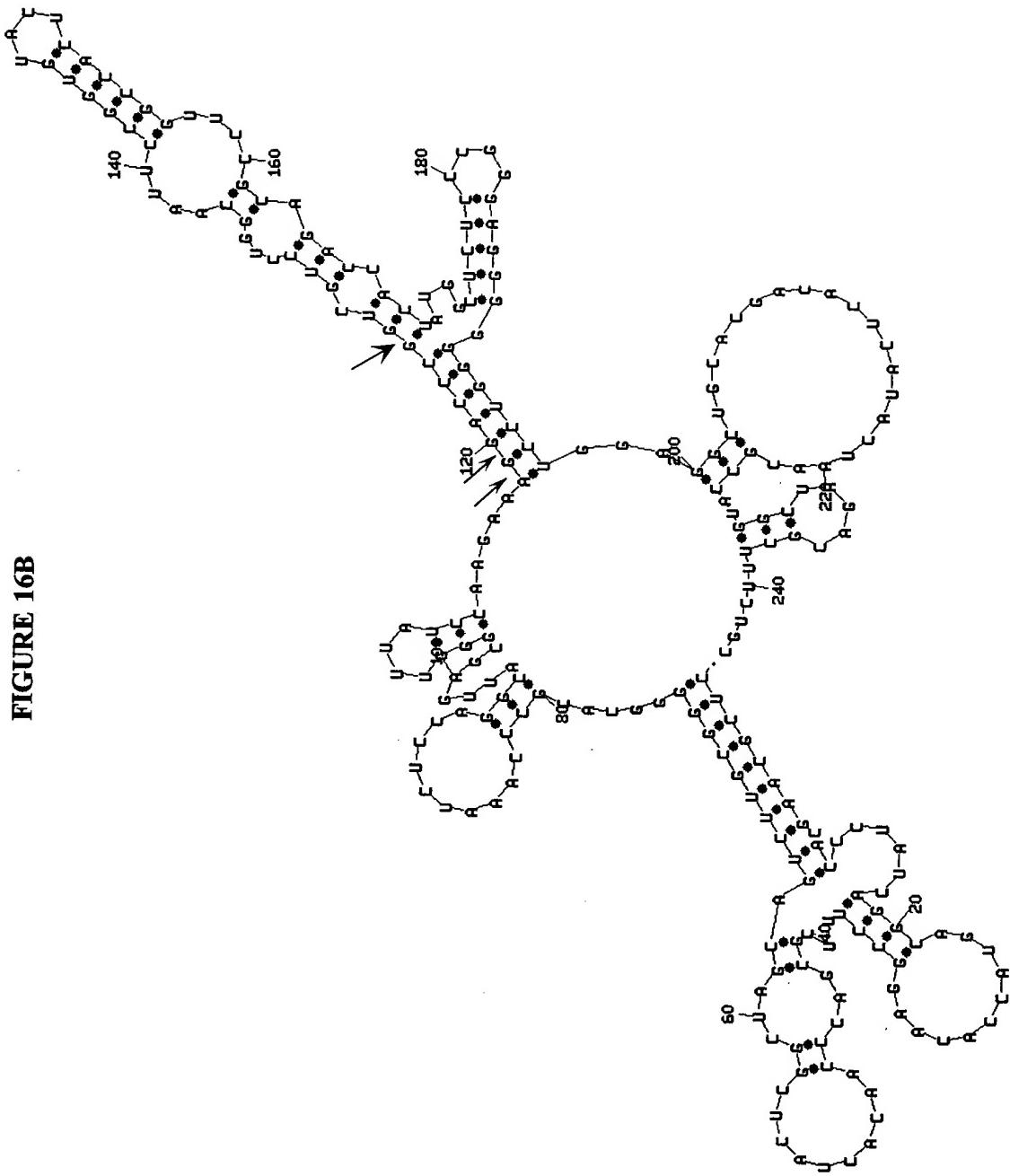


FIGURE 17A

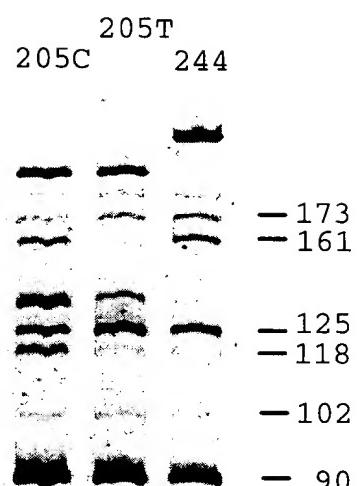


FIGURE 17B

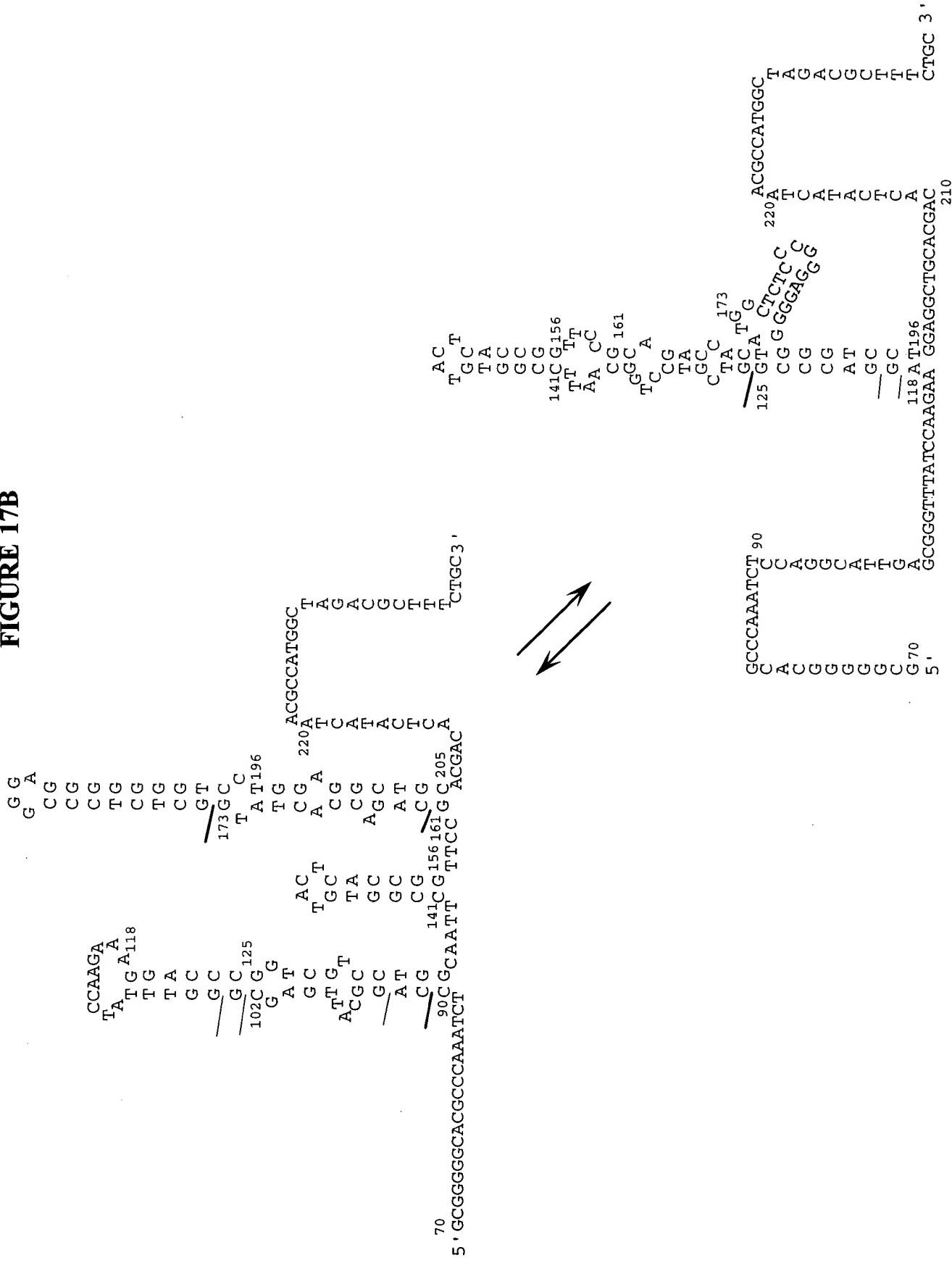


FIGURE 17C

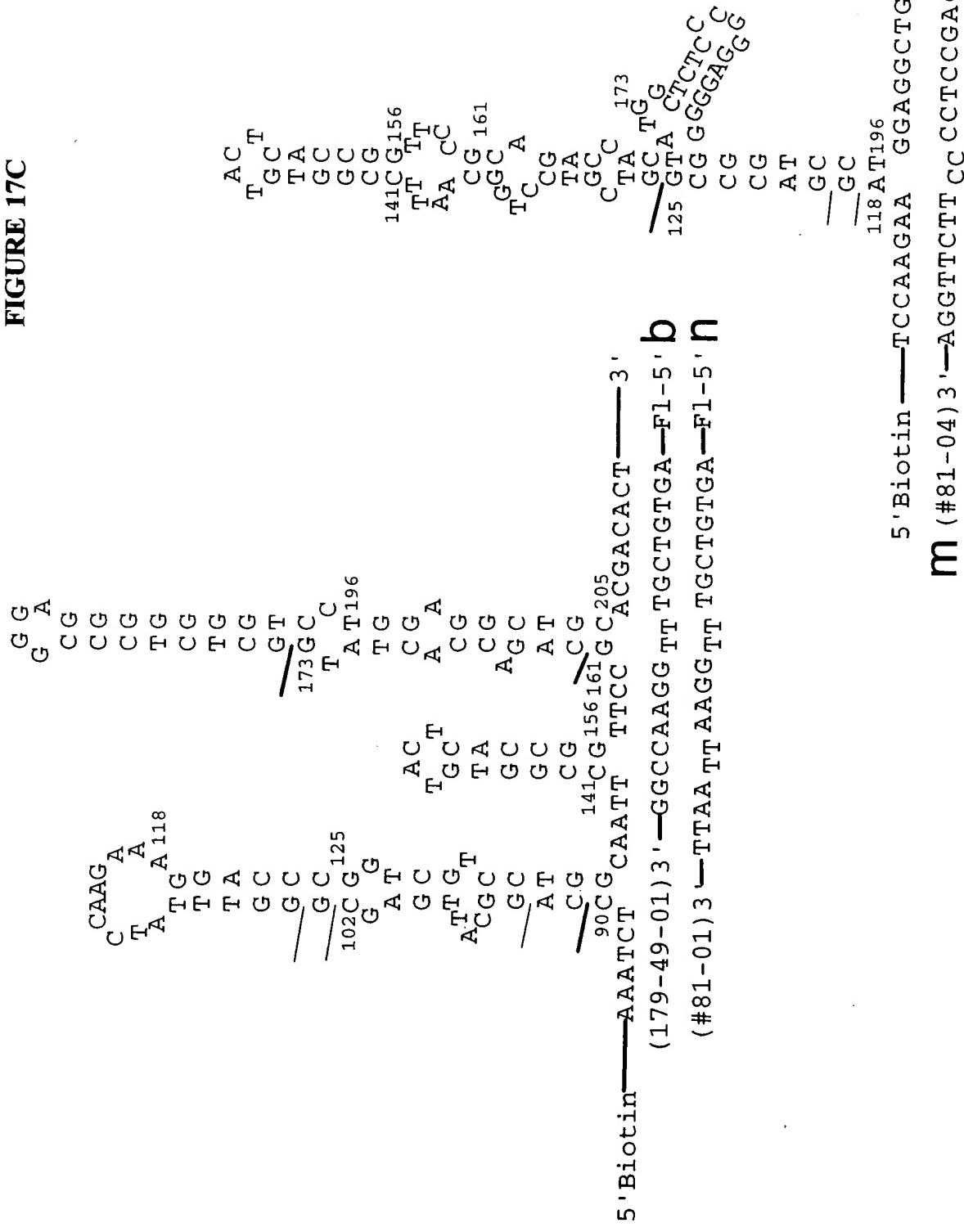


FIGURE 18A**HCV 1a**

G G
G A
C G
C G
C G
T G
C G
T G
C G
T G
C G
G T
G C
173 G C
T C
A T 196
T G
C G
A A
C G
C G
A G C
A T
G C
C G
G C
A T
G C
T G
A C
T G C
T A
A G C
G C
A T
C G
141 C G 156 161 G C 205
90 C G CAATT TTCC ACGACACT — 3'
5' — T G C G G G G C A C G C C C A A A T C T (179-49-01) 3' GGCCAAGG TT TGCTGTGA 5' **b**
(192-72-01) 3' GGCCAAGG AA TGCTGTGA 5' **j**
(192-72-02) 3' GGCCAAGG AC TGCTGTGA 5' **j**
(192-72-03) 3' GGCCAAGG — TGCTGTGA 5' **k**
(192-72-04) 3' GGCCTAGG TT TGCTGTGA 5' **C**
(192-72-05) 3' GGCCAAGG TT TGCAGTGA 5' **d**

FIGURE 18B

HCV 1b

HCV 1b

	G G
	G A
	C G
	C G
T CCAAGA	C G
A A	T G
G G ^{A118}	C G
T G	T G
T A	C G
G C	G T
G C	173 G C
G C	T C
AT 102 C G ¹²⁵	A T ¹⁹⁶
G C ⁷⁰	T G
CG	A T
GC	G C
CG	T AC
TG A T T G T	T G C T
TG C G C T	A A
TG T A	C G
TG G C	C G
CG C A	A G C
CG C	G C
GC A T	A T
GC C G	C G
GC ⁹⁰ C G ¹⁴¹ C G ¹⁵⁶ C G ¹⁶¹ G C ²⁰⁵	ACGACACT - 3'
CAAATCT CAATT TTCC	
(179-49-01) 3' GGCCAAGG <u>TT</u> TGCTGTGA 5' b	
(192-72-01) 3' GGCCAAGG <u>AA</u> TGCTGTGA 5' j	
(192-72-02) 3' GGCCAAGG <u>AC</u> TGCTGTGA 5' j	
(192-72-03) 3' GGCCAAGG — TGCTGTGA 5' k	
(192-72-04) 3' GGC <u>T</u> AGG <u>TT</u> TGCTGTGA 5' C	
(192-72-05) 3' GGCCAAGG <u>TT</u> TGC <u>AGT</u> GA 5' d	

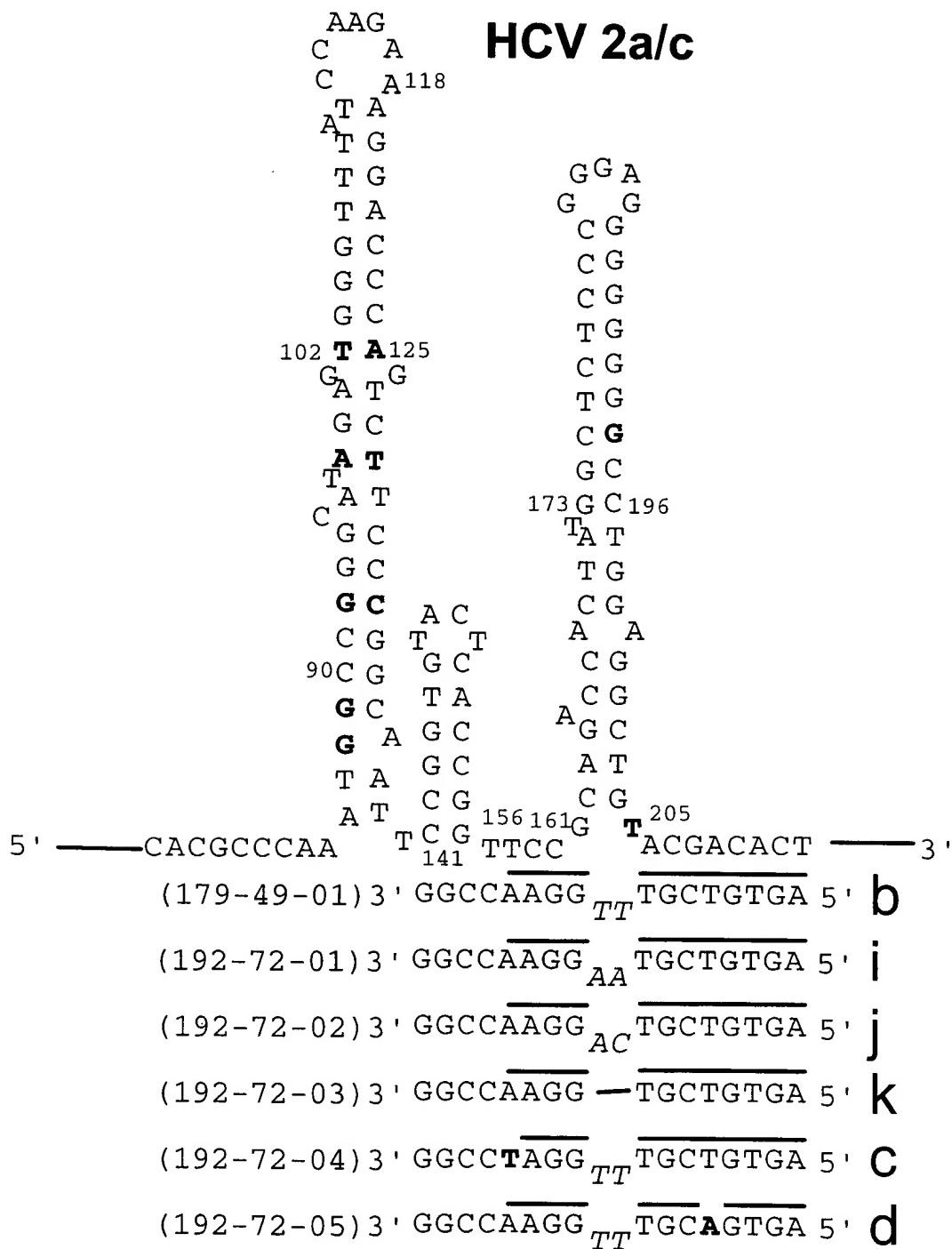
FIGURE 18C

FIGURE 18D**HCV 3a**

CAAG
C A

T A	G A		
T A 118	G G		
G G	C G		
T G	C G		
T A	C G		
G C	C G		
G C	T G		
G C	C G		
102 C G 125	T G		
G G	C T		
A T	G C		
G C	173 G C		
A T T A C	T A T 196		
T G C	T G		
G C	C G		
G C T T	A A		
T A G C	C G		
90 C G	T A		
T G C G C	C G		
T G G C	A G C		
T A G C	A T		
A T C G	C G		
A T C G 156 161	G C 205		
5' — CACGCCCA	TTCC	ACGACACT	— 3'
(179-49-01) 3'	GGCCAAGG	<u>TT</u> TGCTGTGA	5' b
(192-72-01) 3'	GGCCAAGG	<u>AA</u> TGCTGTGA	5' i
(192-72-02) 3'	GGCCAAGG	<u>AC</u> TGCTGTGA	5' j
(192-72-03) 3'	GGCCAAGG	— <u>TGCTGTGA</u> 5' k	
(192-72-04) 3'	GGCCTAGG	<u>TT</u> TGCTGTGA	5' C
(192-72-05) 3'	GGCCAAGG	<u>TT</u> TGC A GTGA	5' d

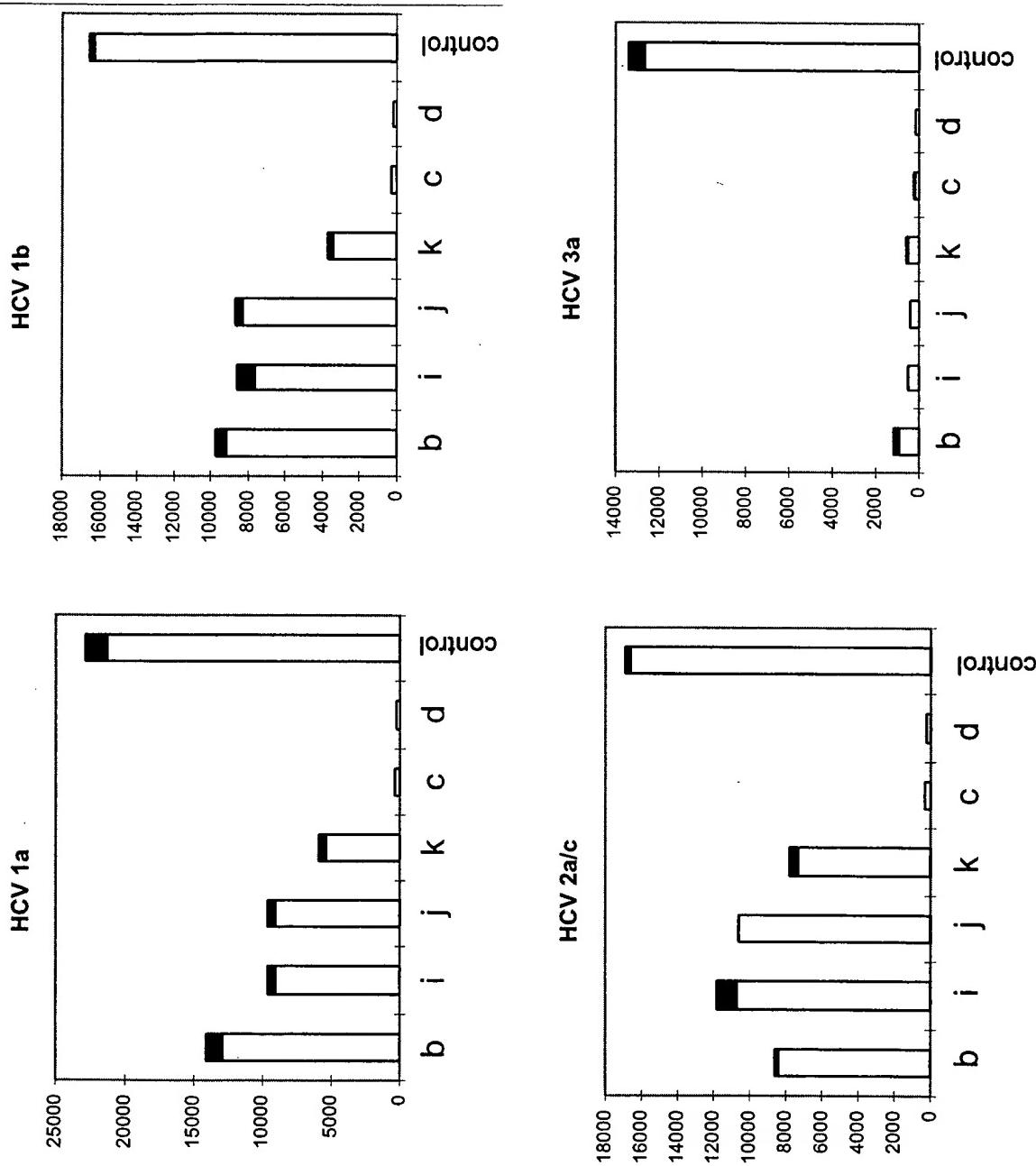
FIGURE 19

FIGURE 20A

G G
G A
C G
C G
C G
T G
C G
T G
C G
G T
173 G C
T A T 196
T G
C G
A A
C G
C G
A G C
A T
C G
G C²⁰⁵
A C G A C A C T — 3'

HCV 1a

- 3' - G GCC A AG G C G G T C T G G T G A - F 1 ' 5' (205-13-02) **a**
 3' - G GCC A AG G T T T G C T G T G A - F 1 ' 5' (179-49-01) **b**
 3' - G GCC T A G G T T T G C T G T G A - F 1 ' 5' (192-72-04) **c**
 3' - G GCC A AG G T T T G C A G T G A - F 1 ' 5' (192-72-05) **d**
 3' - G GCC A AG G - F 1 5' (205-27-01) **e**

FIGURE 20B

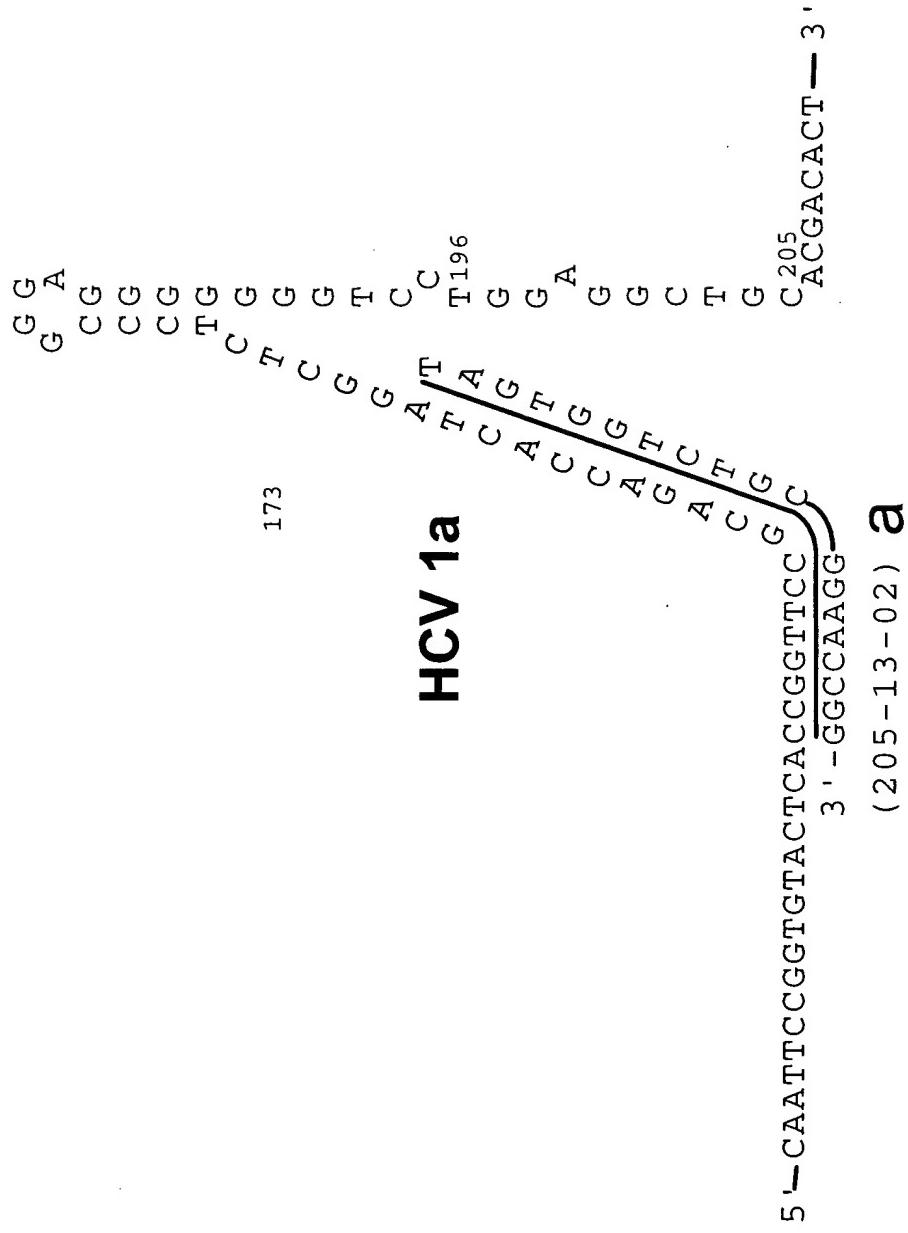


FIGURE 21

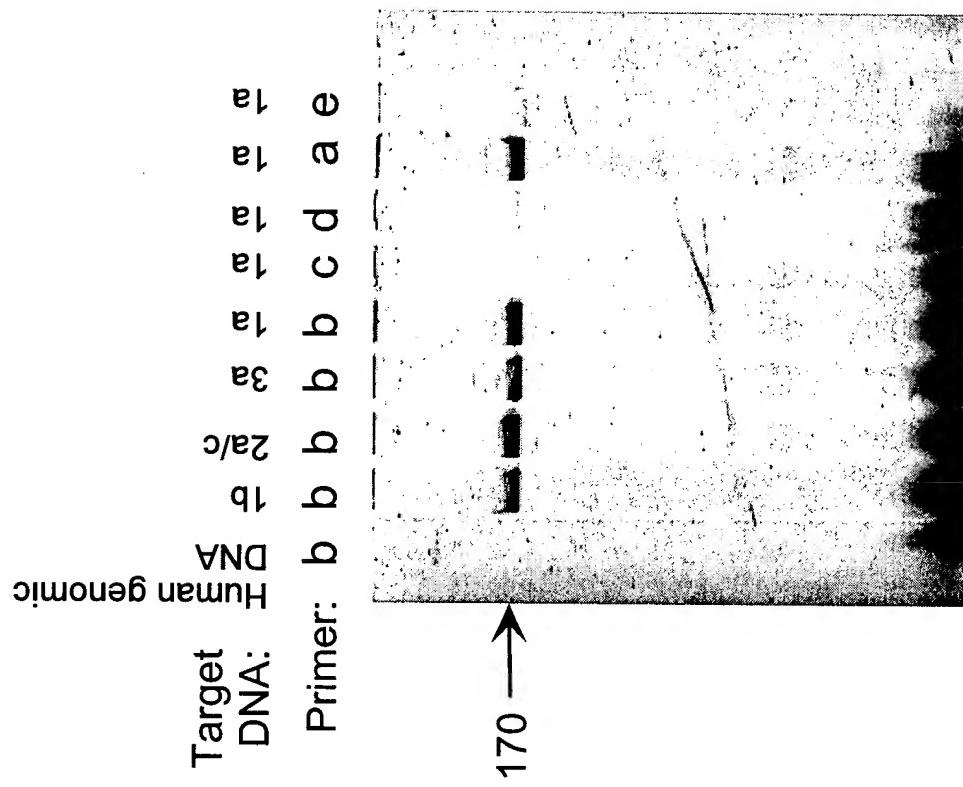
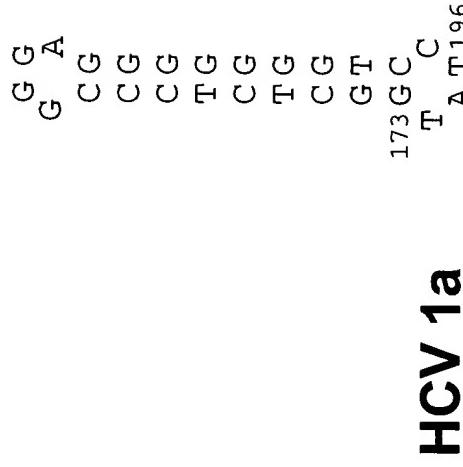


FIGURE 22

3' —GGCCAAGGGTCTGGTGA—F1' 5' (205-13-02) **a**

3' —GGCCAAGGTTTGCTGTA—F1' 5' (179-49-01) **b**

3' —GGCCAAGG-F15' (205-27-01) **e**

FIGURE 23

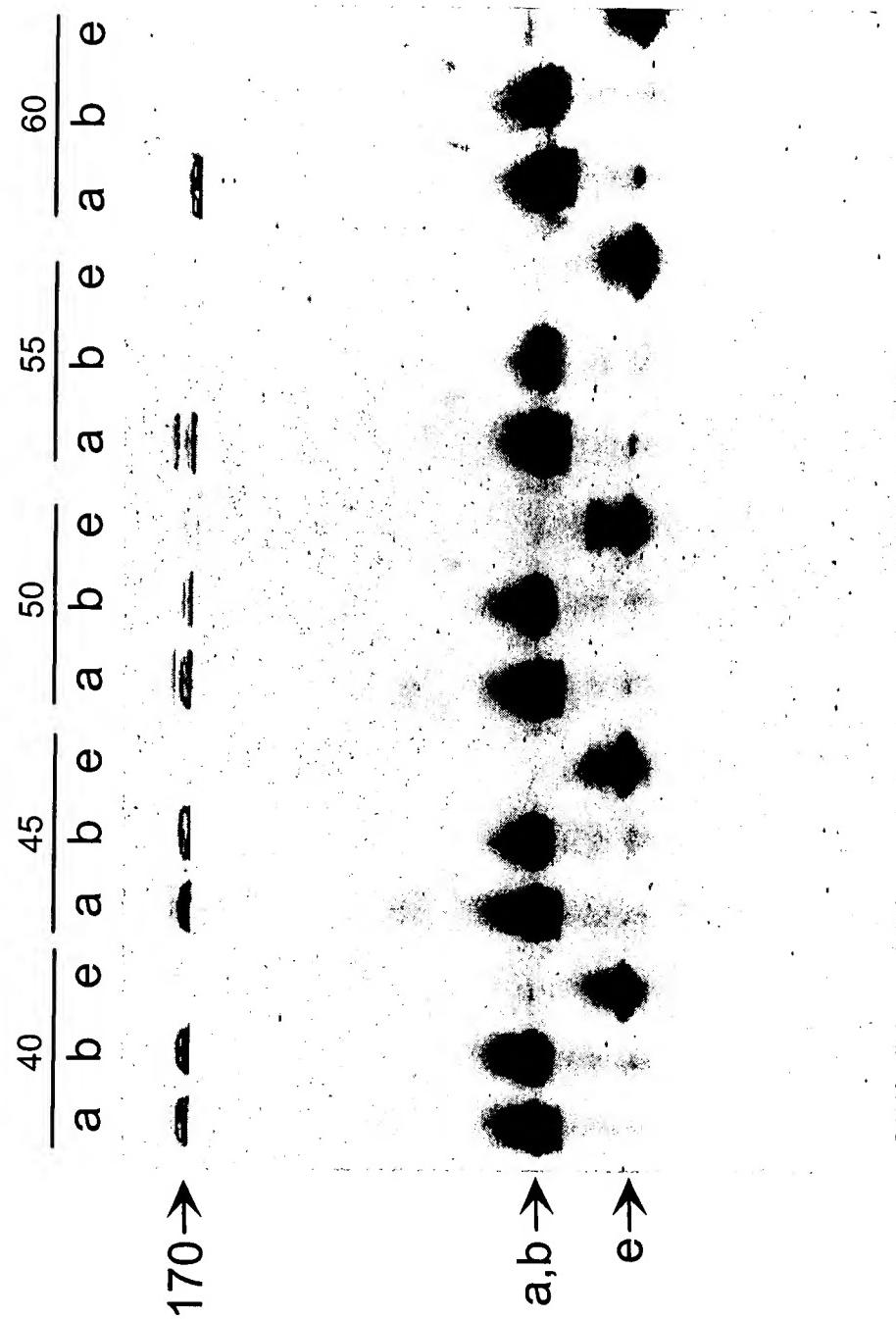


FIGURE 24

G G
 G A
 C G
 C G
 C G
 T G
 C G
 T G
 C G
 G T
 173 G C
 T A T₁₉₆ C

HCV 1a

T G
 C G
 A A
 C G
 C G
 A G C
 A T
 C G

5'—CAATTCCGGTGTACTCACCGGTTCC G C²⁰⁵ ACGACACT— 3'

- f** (192-96-01) 3' —TAAGGCCACATGAGT— 5'
- a** 3' —GGCCAAGGCCGTCTGGTGA—F1' 5' (205-13-02)
- b** 3' —GGCCAAGG T_T TGCTGTGA—F1' 5' (179-49-01)
- c** 3' —GGCCTAGG T_T TGCTGTGA—F1' 5' (192-72-04)
- d** 3' —GGCCAAGG T_T TGCAGTGA—F1' 5' (192-72-05)
- e** 3' —GGCCAAGG—F15' (205-27-01)

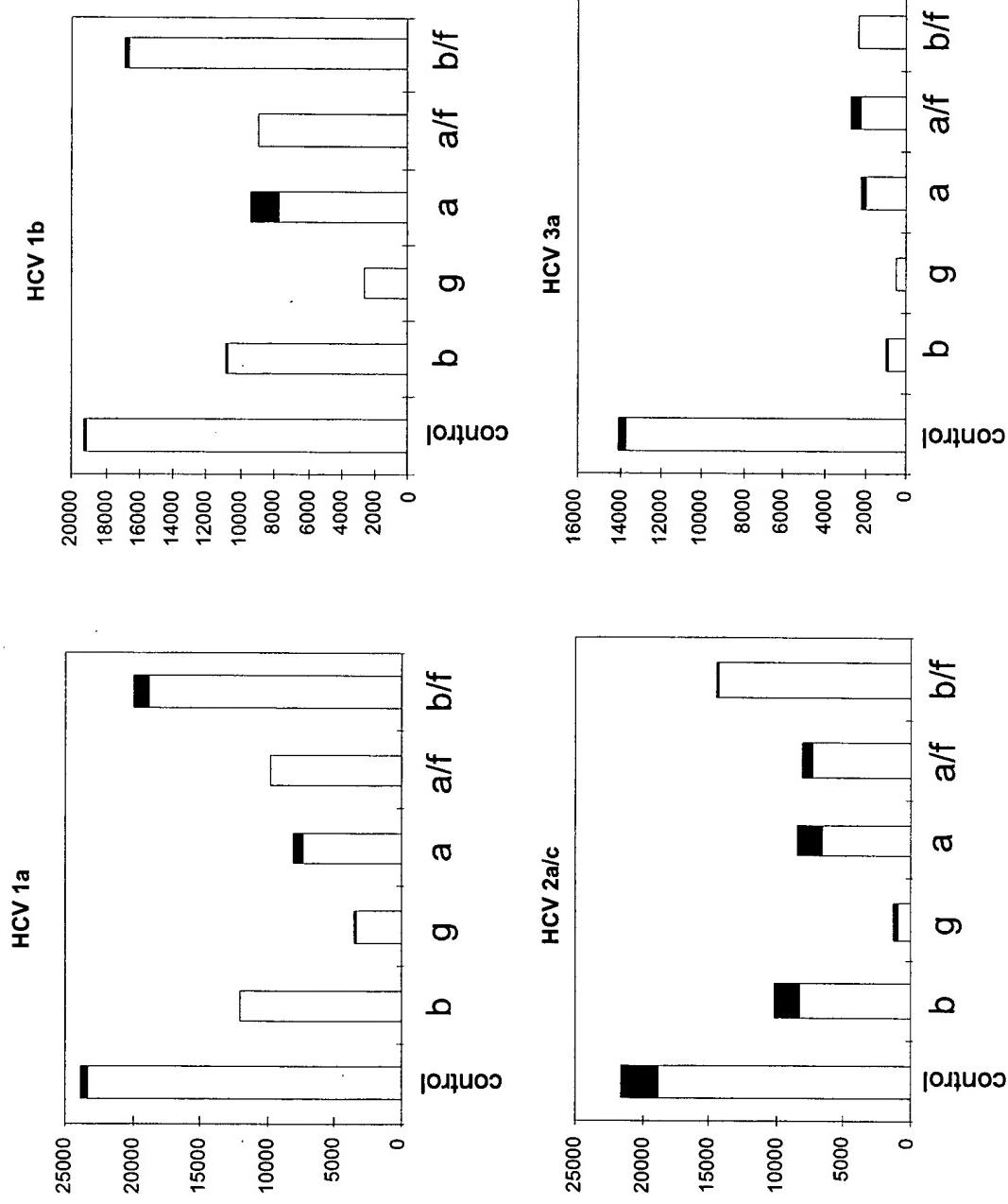
FIGURE 25

FIGURE 26

5' -ATTCCGGTGTACTCACCGGTTCCAAACGACACT-3' (205-13-01) **S.T.**

f (192-96-01) 3' -TAAGGCCACATGAGT-5'

3' -GGCCAAGGGTCTGGTGA-F1' 5' (205-13-02) **a**

3' -GGCCAAGG TT TGCTGTGA-F1' 5' (179-49-01) **b**

3' -GGCCTAGG TT TGCTGTGA-F1' 5' (192-72-04) **c**

3' -GGCCAAGG TT TGCAGTGA-F1' 5' (192-72-05) **d**

3' -GGCCAAGG-F1 5' (205-27-01) **e**

FIGURE 27

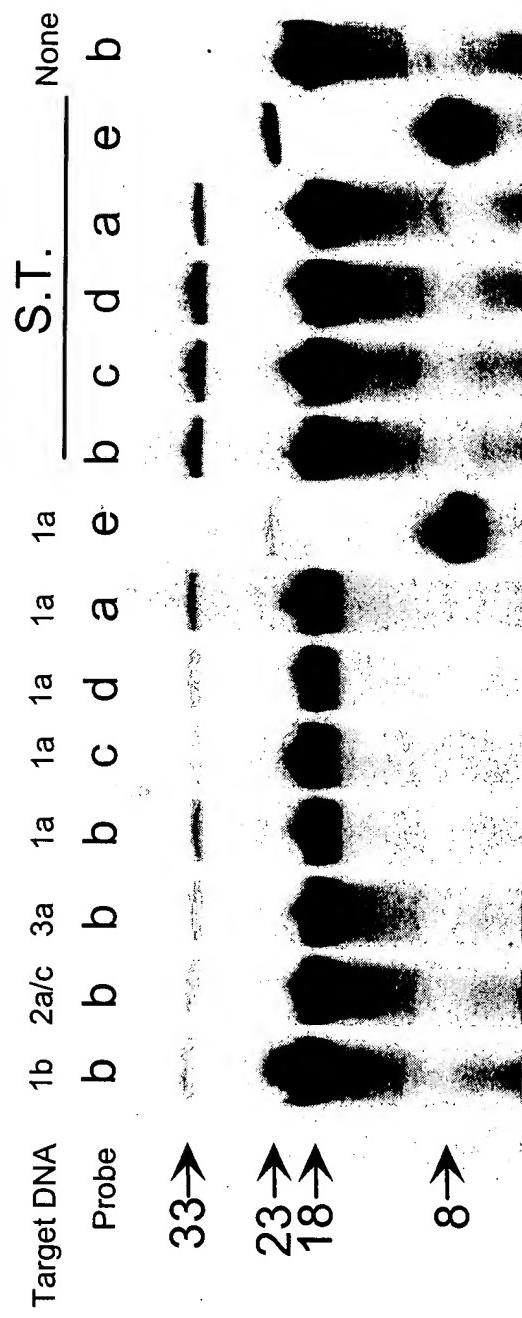


FIGURE 28

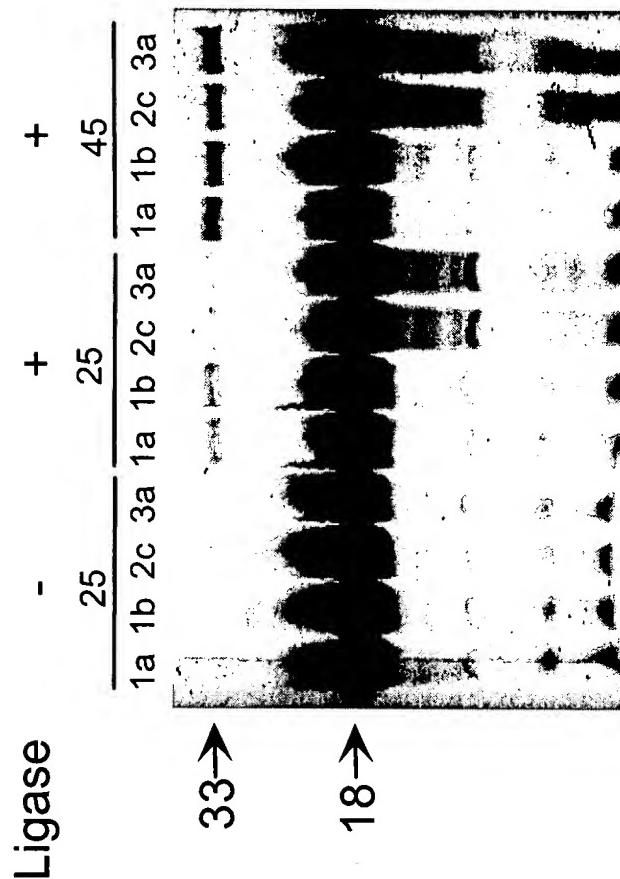
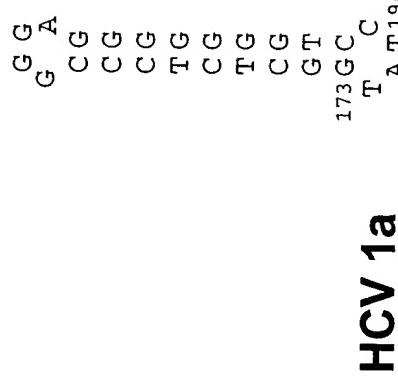


FIGURE 29A

5' - CAAATTCCGGTGTAC'TCACCGGTTCC' G C²⁰⁵ ACGACACT — 3'
 3' - GCCCAAGG_{TT} TGCTGTGA-F1' 5' (205-13-02) **a**
 3' - GCCCAAGG_{TT} TGCTGTGA-F1' 5' (179-49-01) **b**
 3' - GGCCTAGG_{TT} TGCTGTGA-F1' 5' (192-72-04) **c**
 3' - GCCCAAGG_{TT} TGCAGTGA-F1' 5' (192-72-05) **d**
 3' - GCCCAAGG-F15' (205-27-01) **e**
g 3' - TAAGGCCACATGAGTG_{TT} T_T T_{F1}' 5' (192-96-02)

FIGURE 29B

5' - ATTCCGGTGTACTCACCGGTTCCAAACGACACT-3' (205-13-01) **S.T.**
3' - GCCCAAGCGTCTGGTGA-F1 5' (205-13-02) **a**

3' - GCCCAAGG TT TGCTGTTGA-F1 5' (179-49-01) **b**

3' - GGCCTAGG TT TGCTGTTGA-F1 5' (192-72-04) **c**

3' - GCCCAAGG TT TGCAAGTGA-F1 5' (192-72-05) **d**

3' - GCCCAAGG-F15 5' (205-27-01) **e**

3' - TAAAGGCCACATGAGTG TT-F1 5' (192-96-02) **g**

FIGURE 30



FIGURE 31G G
G A

C G

C G

C G

C G

T G

C G

T G

C G

C G

G T

173 G C

T A T 196 C

HCV 1a

T G

C G

A A

C G

C G

A G C

A T

C G

A T

C G

A C G A C A C T — 3'

5'—CAATTCCGGTACTCACCGGTTCC G C²⁰⁵ ACGACACT—3'3'—G GCCAAGG TT TGCTGTGA—F1' 5' (179-49-01)h (10 bp) 3'—CACATGAGTG TT T_T_T_{F1}' 5' (205-81-01)**b**

FIGURE 32

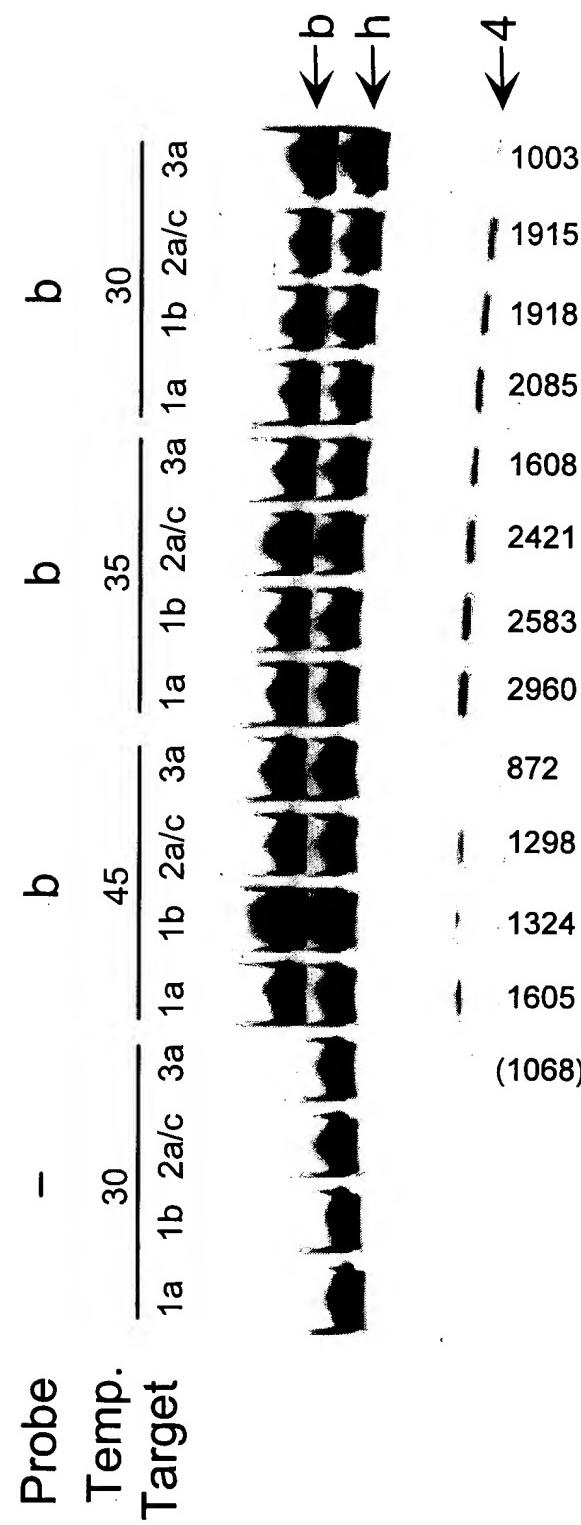


FIGURE 33

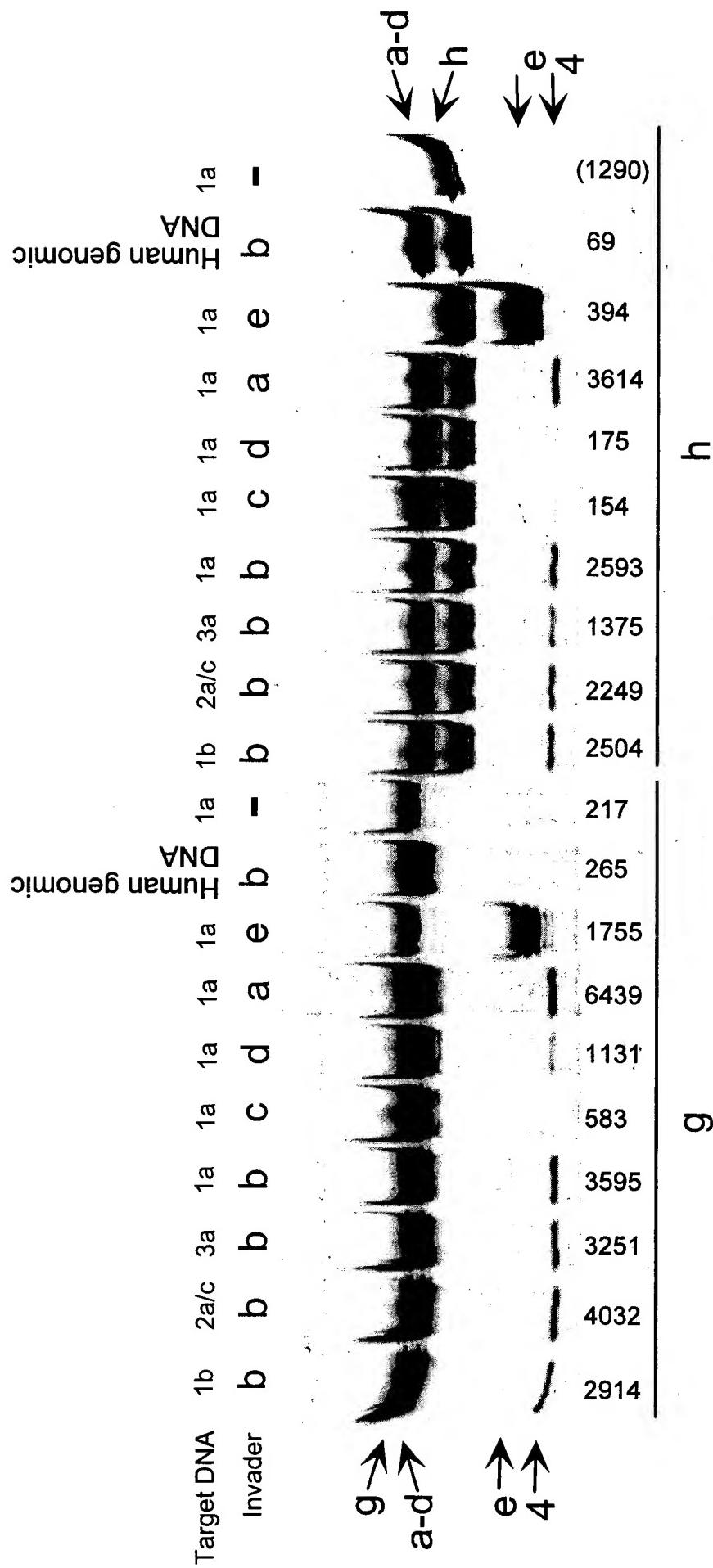


FIGURE 34

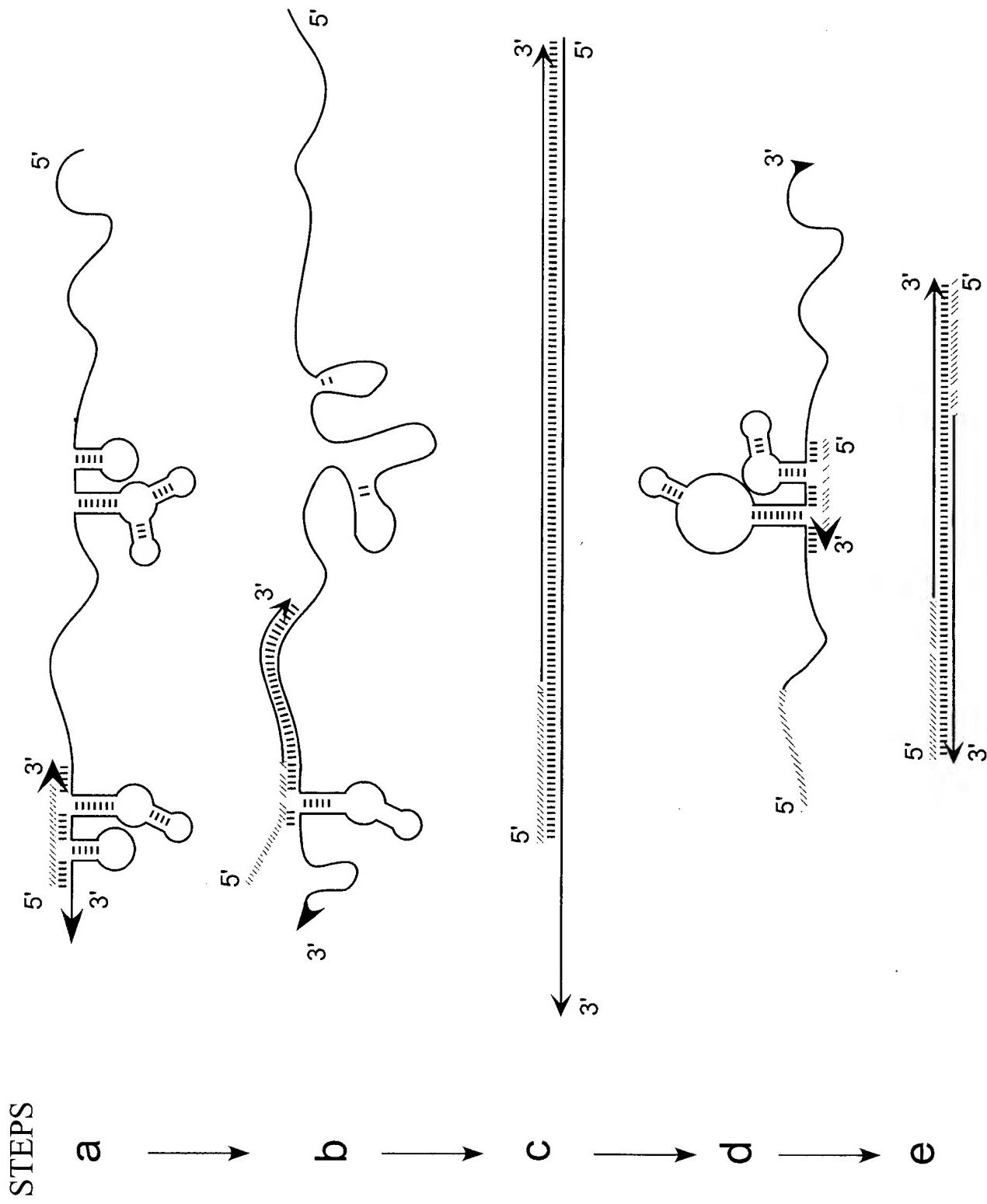


FIGURE 35

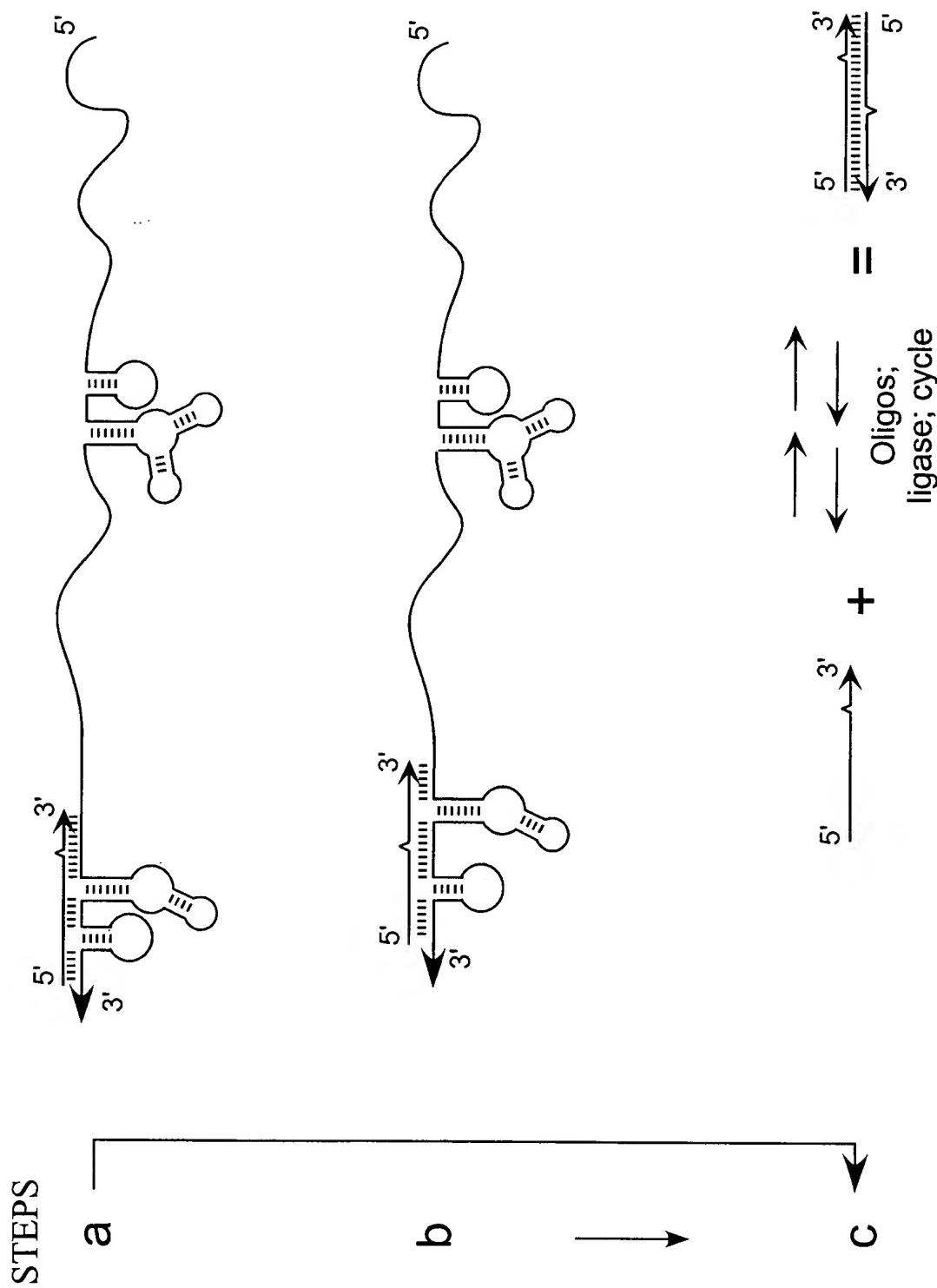


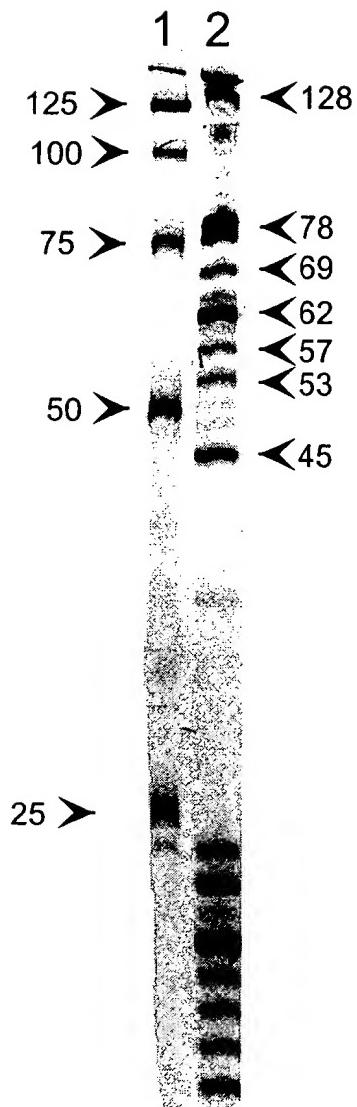
FIGURE 36

FIGURE 37A

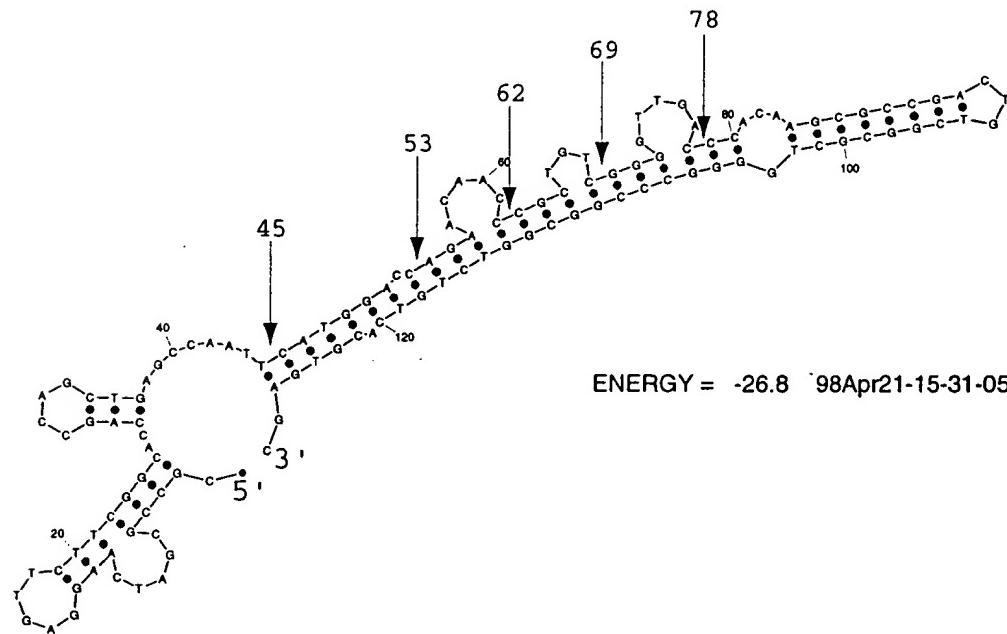
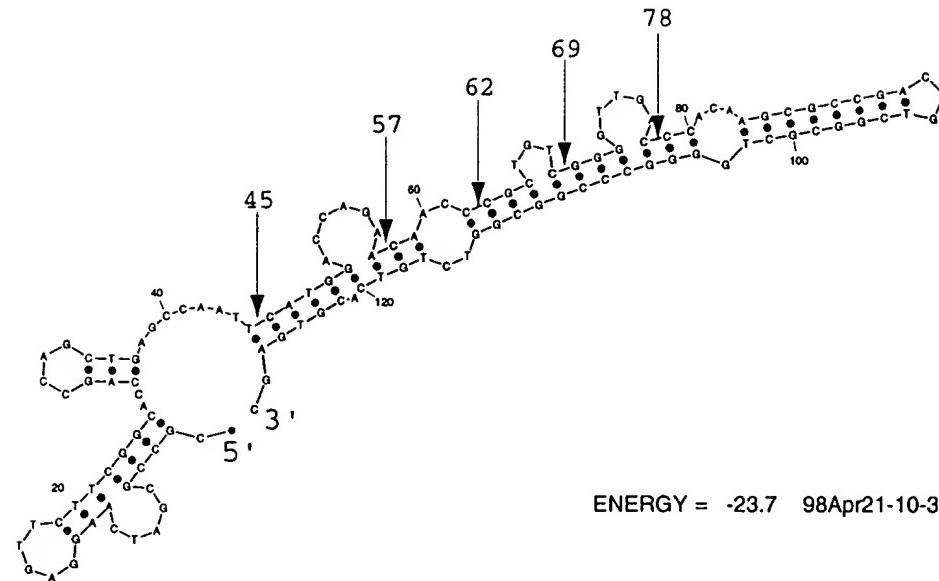


FIGURE 37B

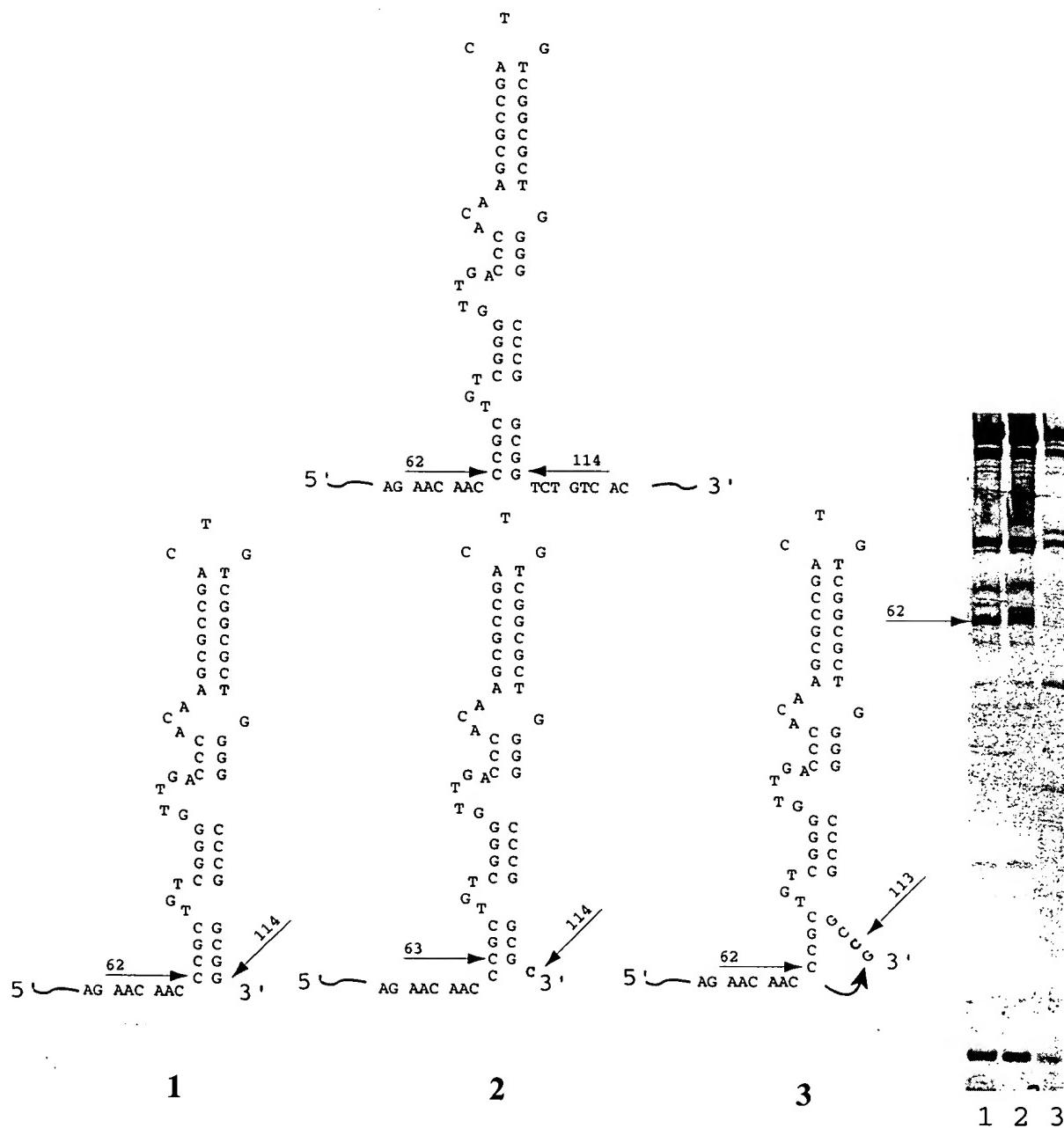


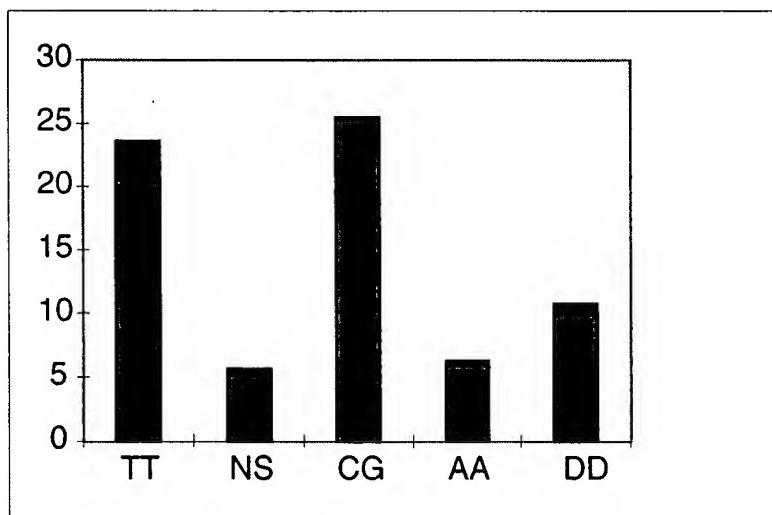
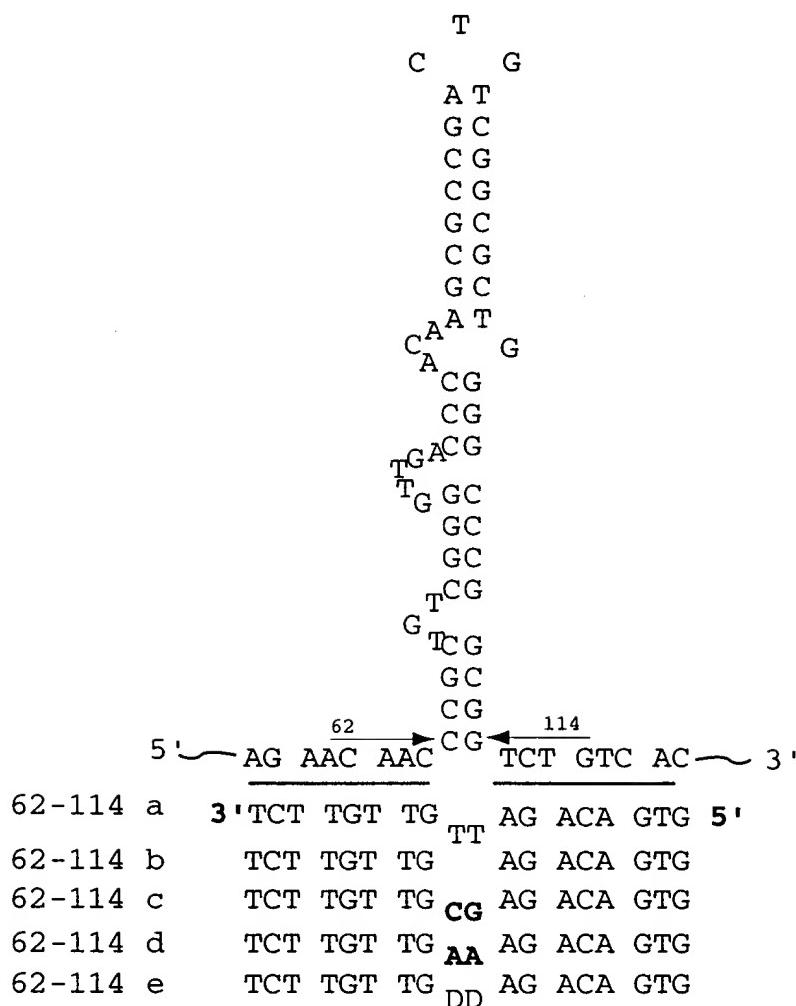
FIGURE 37C

FIGURE 38A

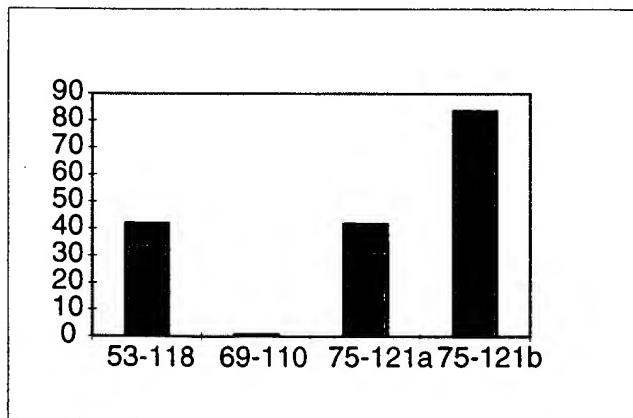
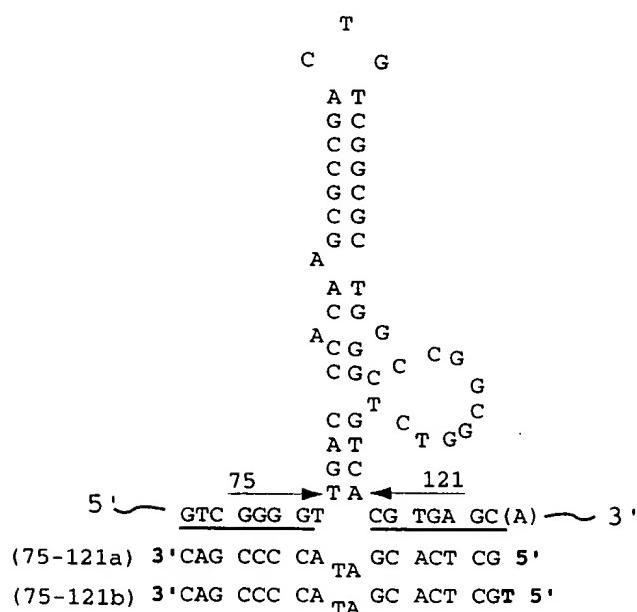
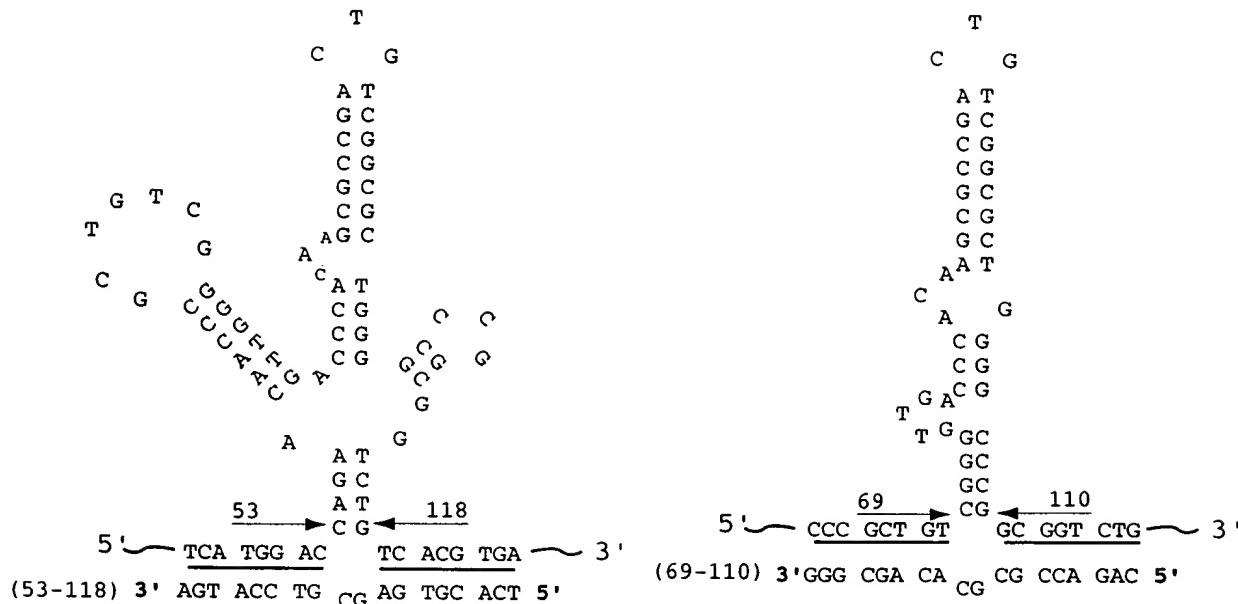


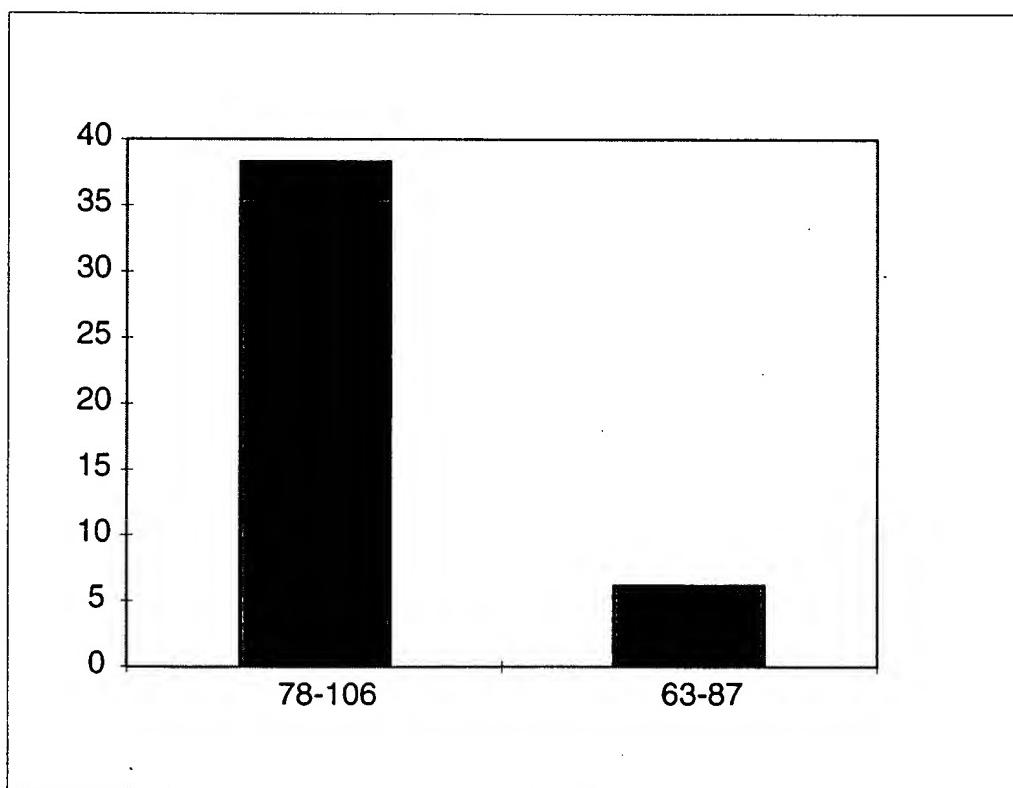
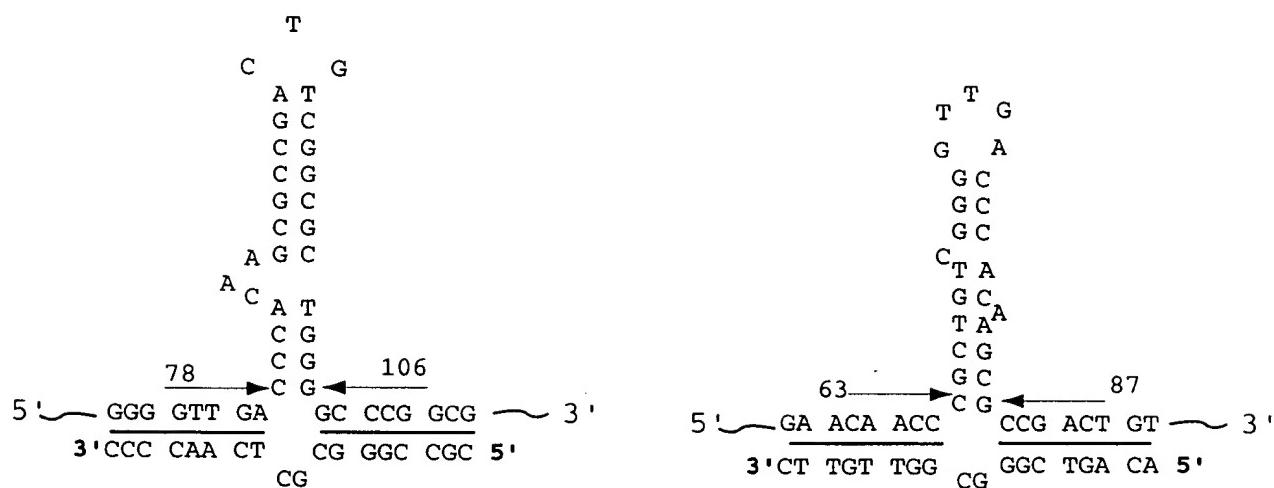
FIGURE 38B

FIGURE 38C

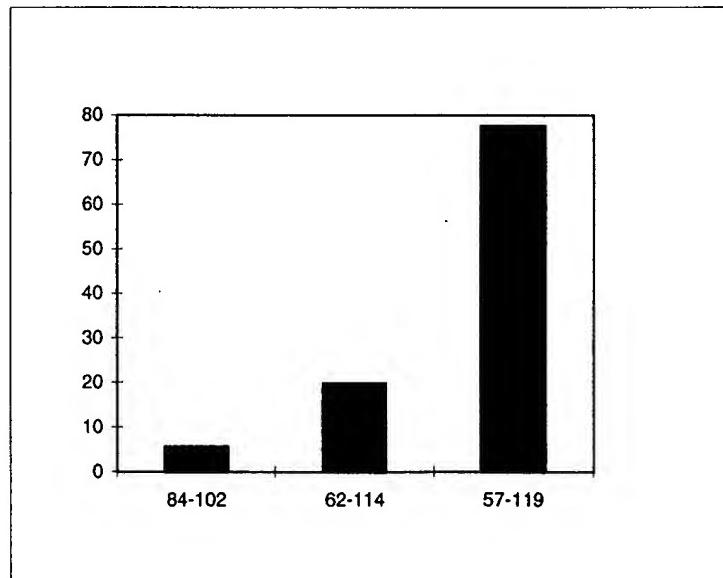
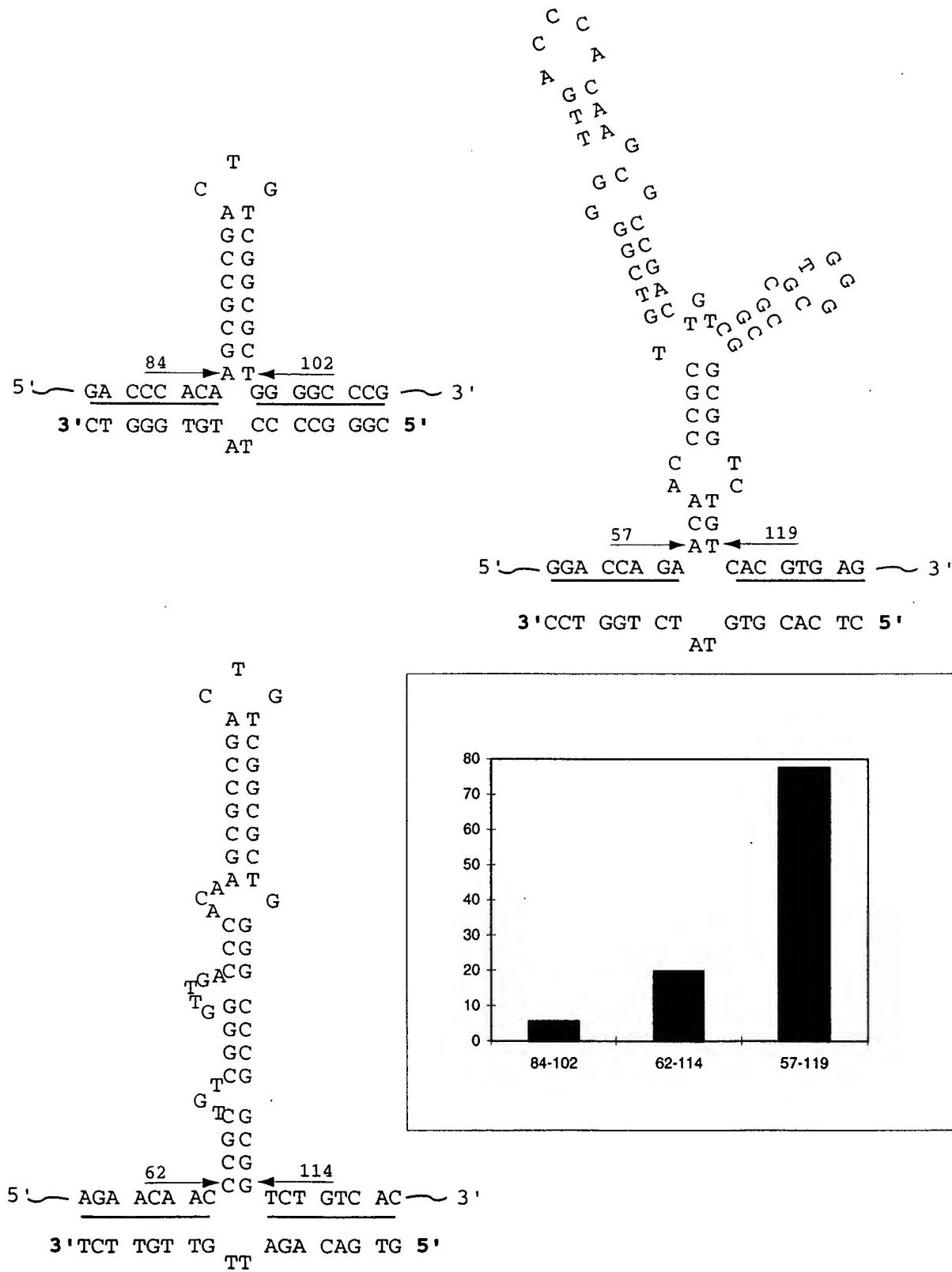


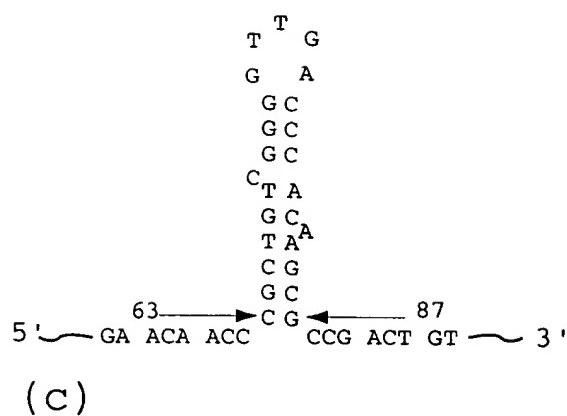
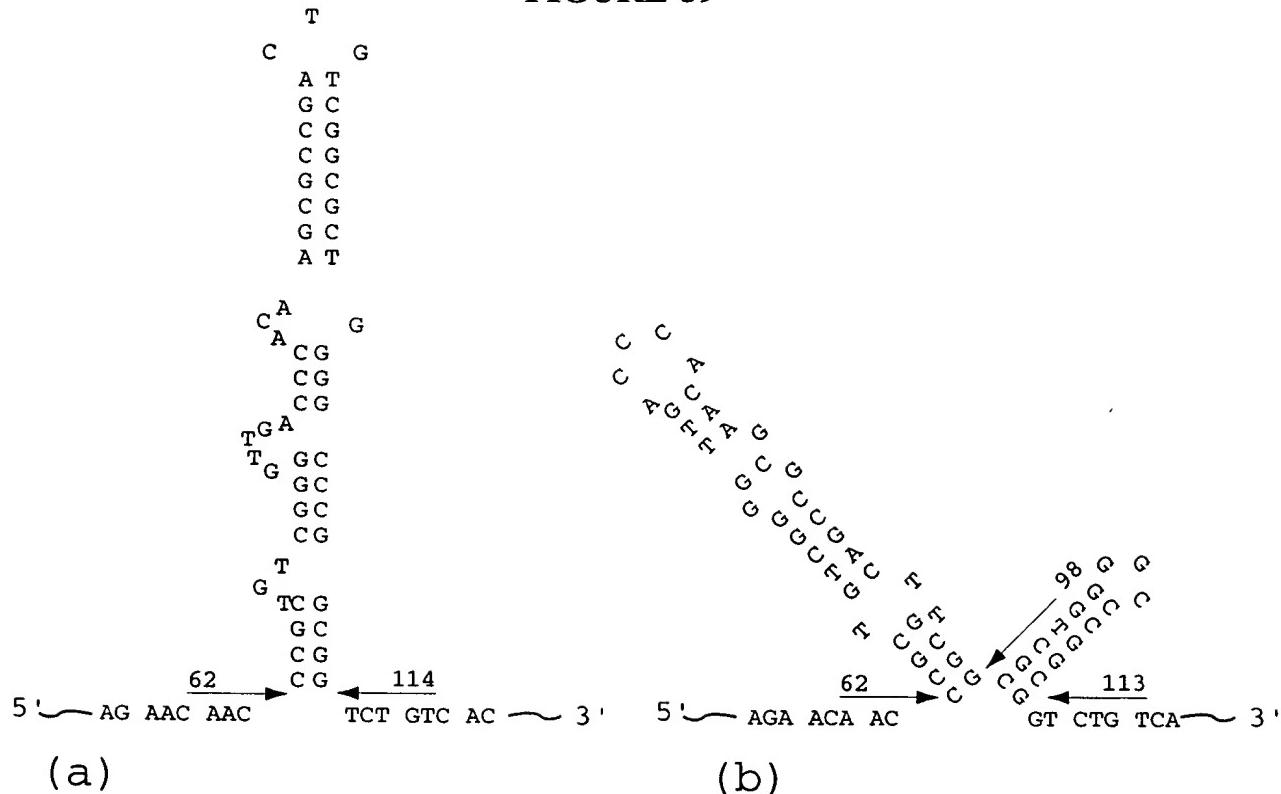
FIGURE 39

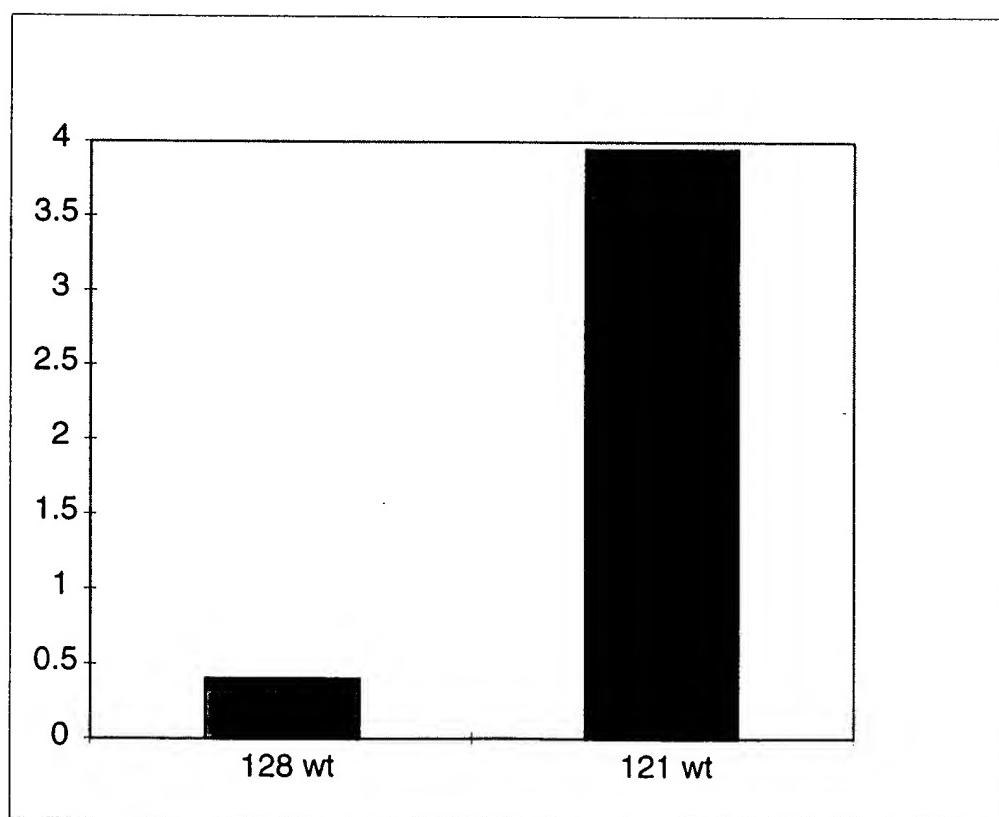
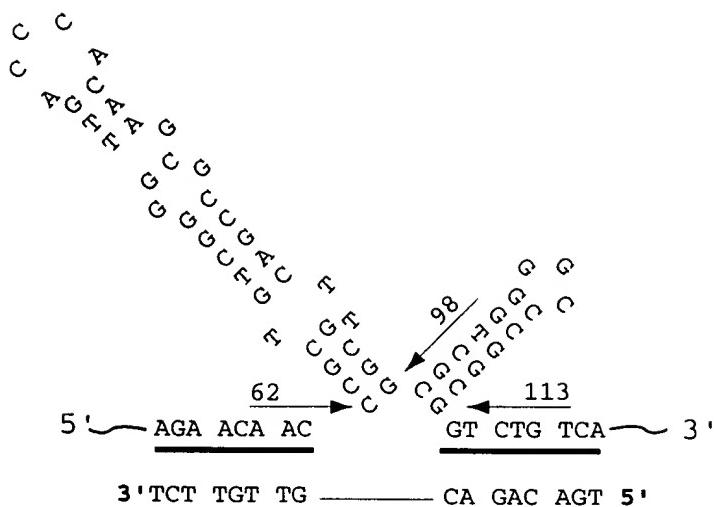
FIGURE 40

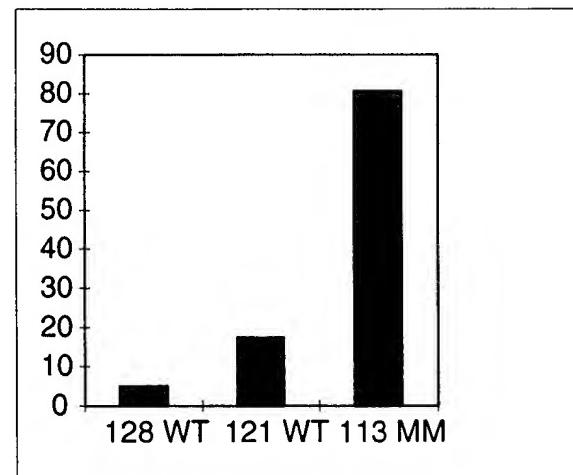
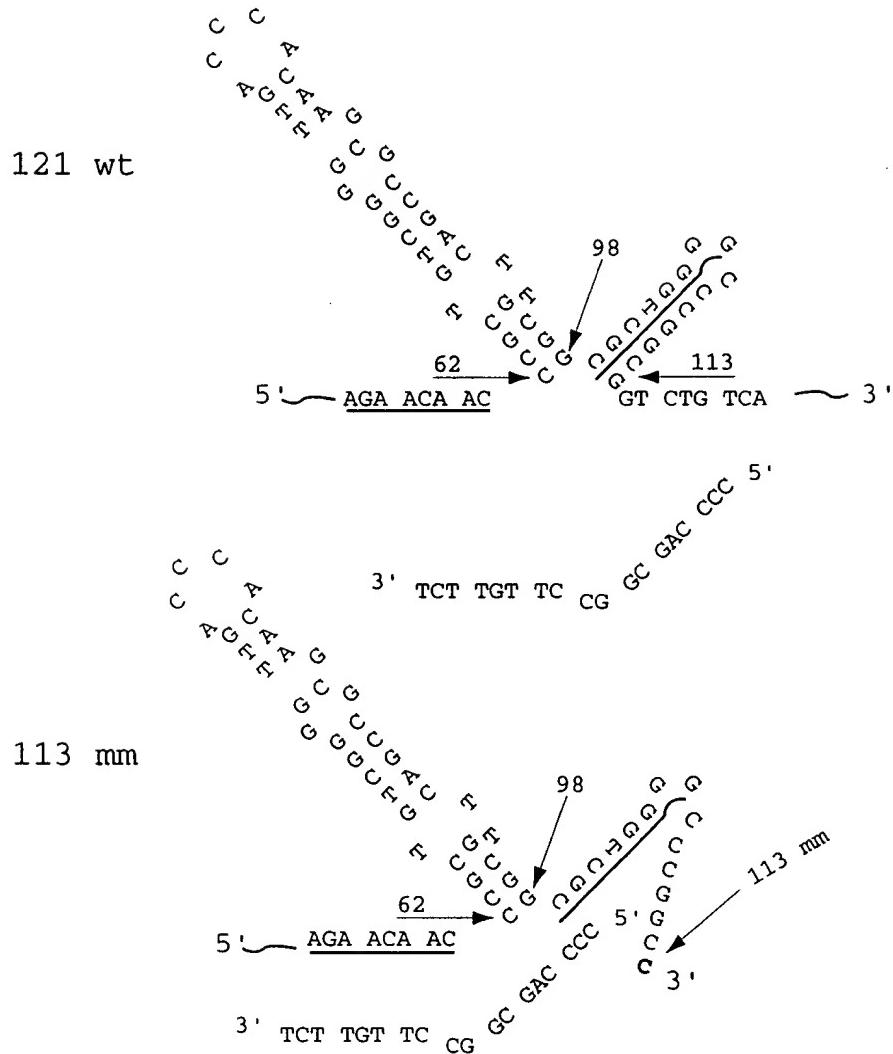
FIGURE 41

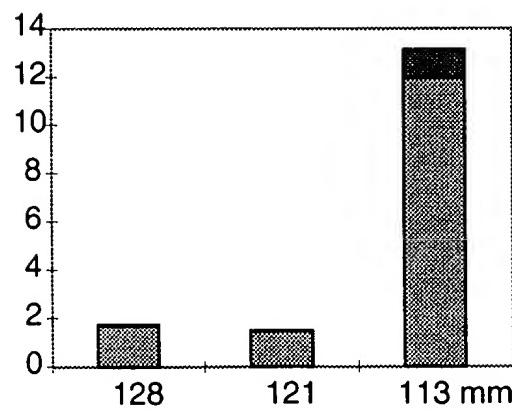
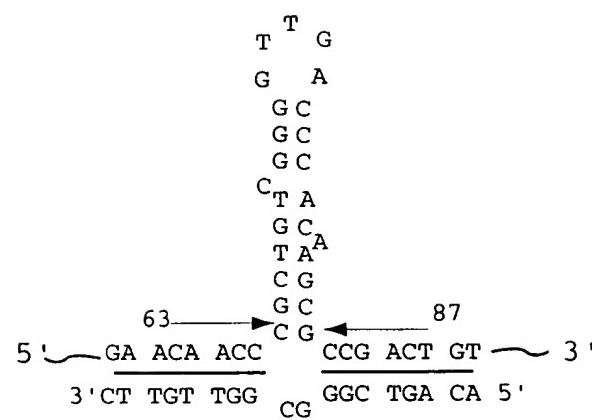
FIGURE 42

FIGURE 43A

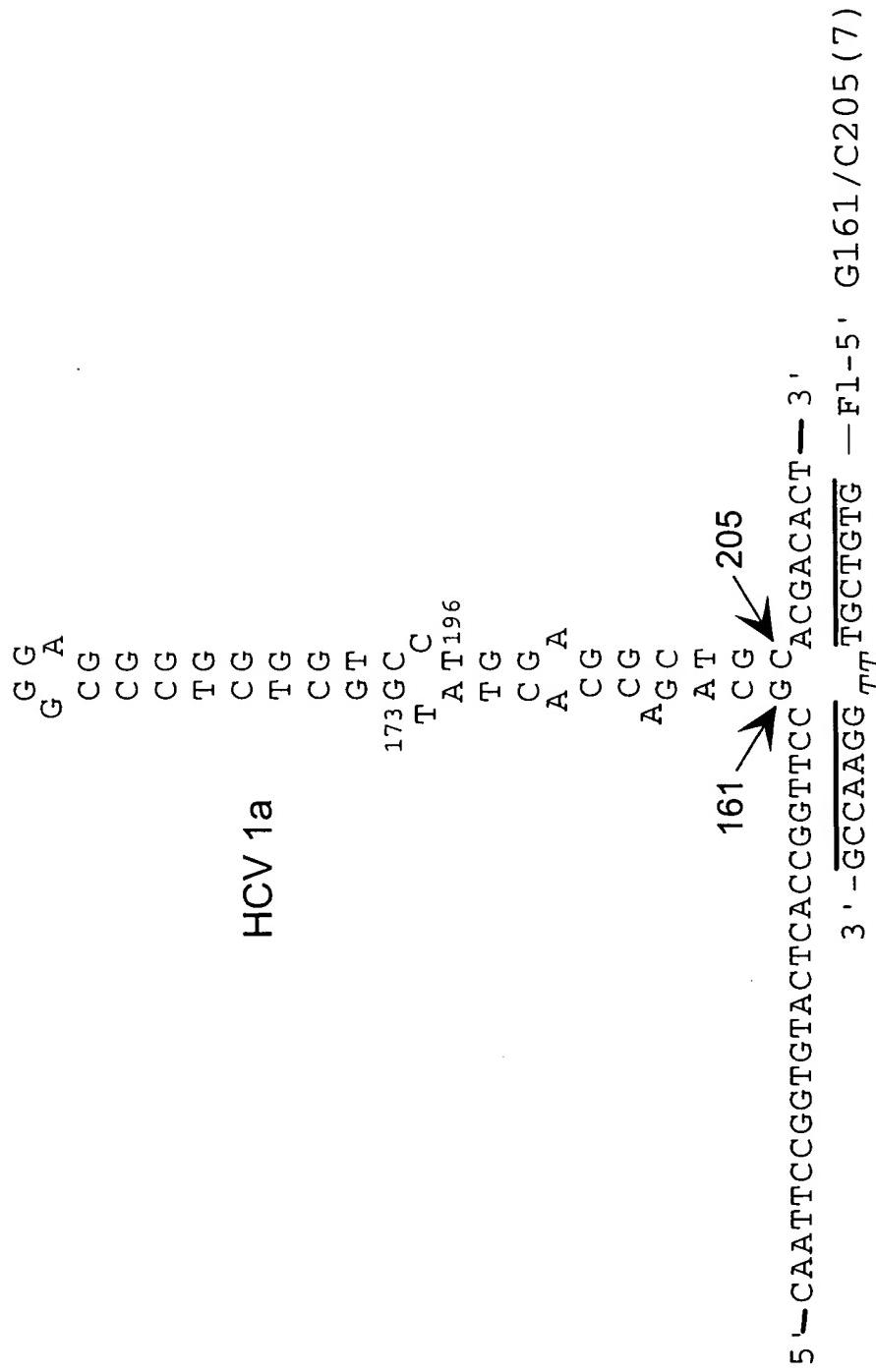


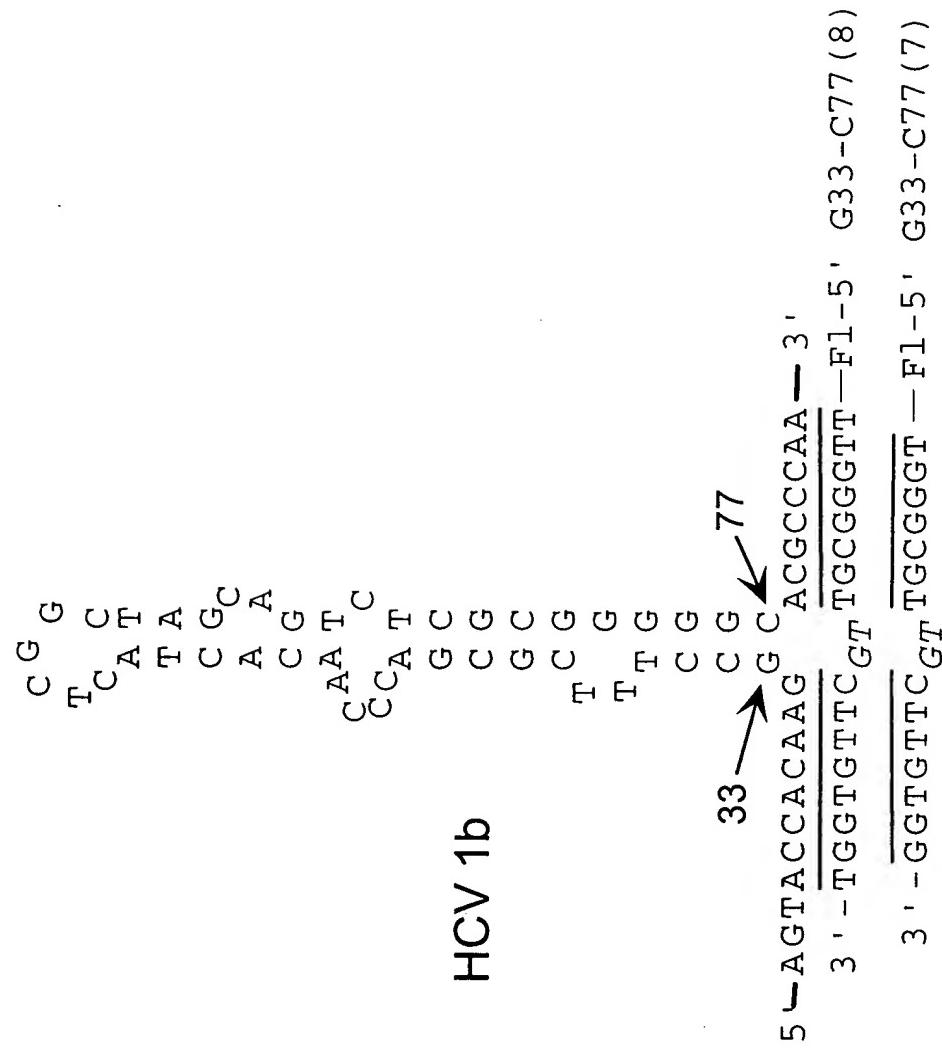
FIGURE 43B

FIGURE 44A

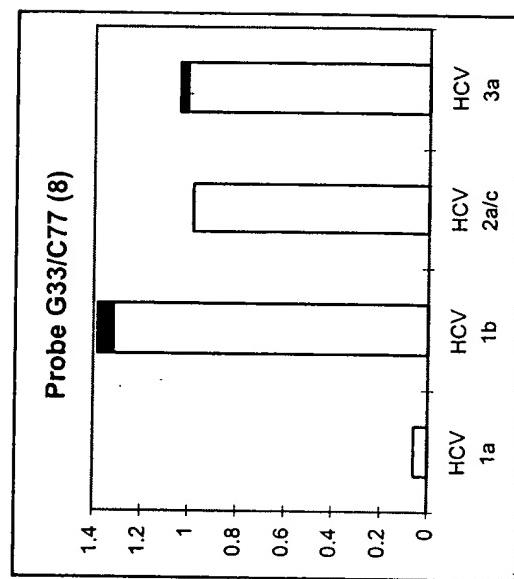
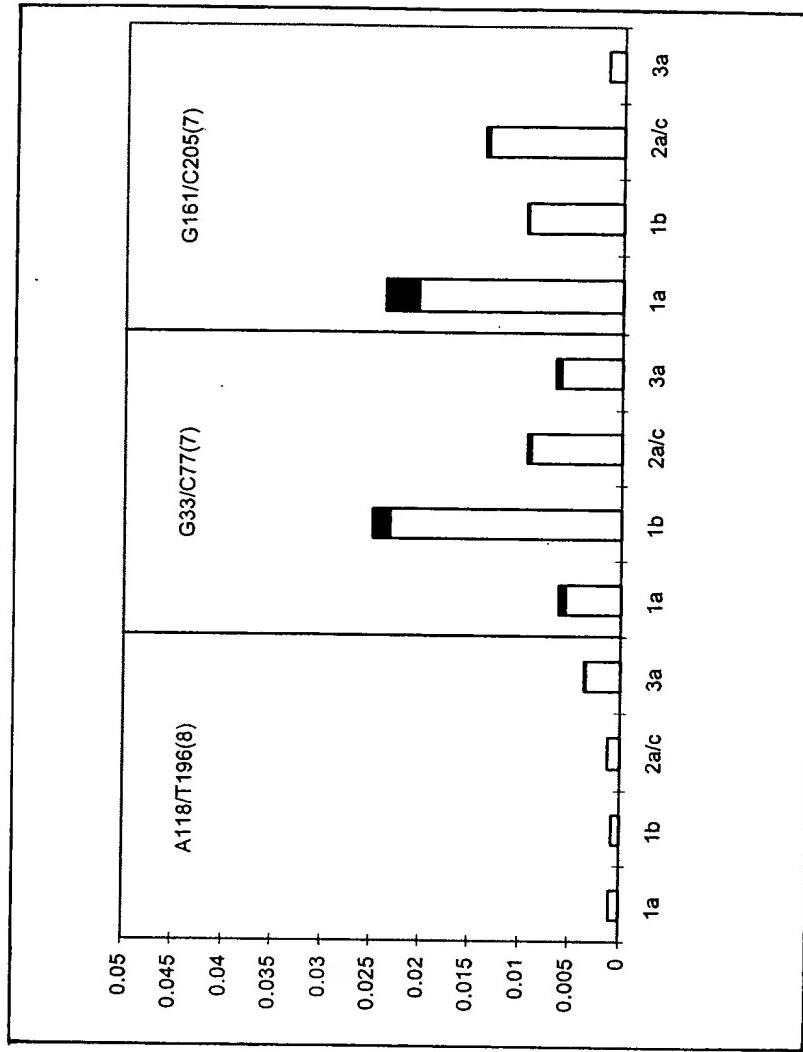


FIGURE 44B



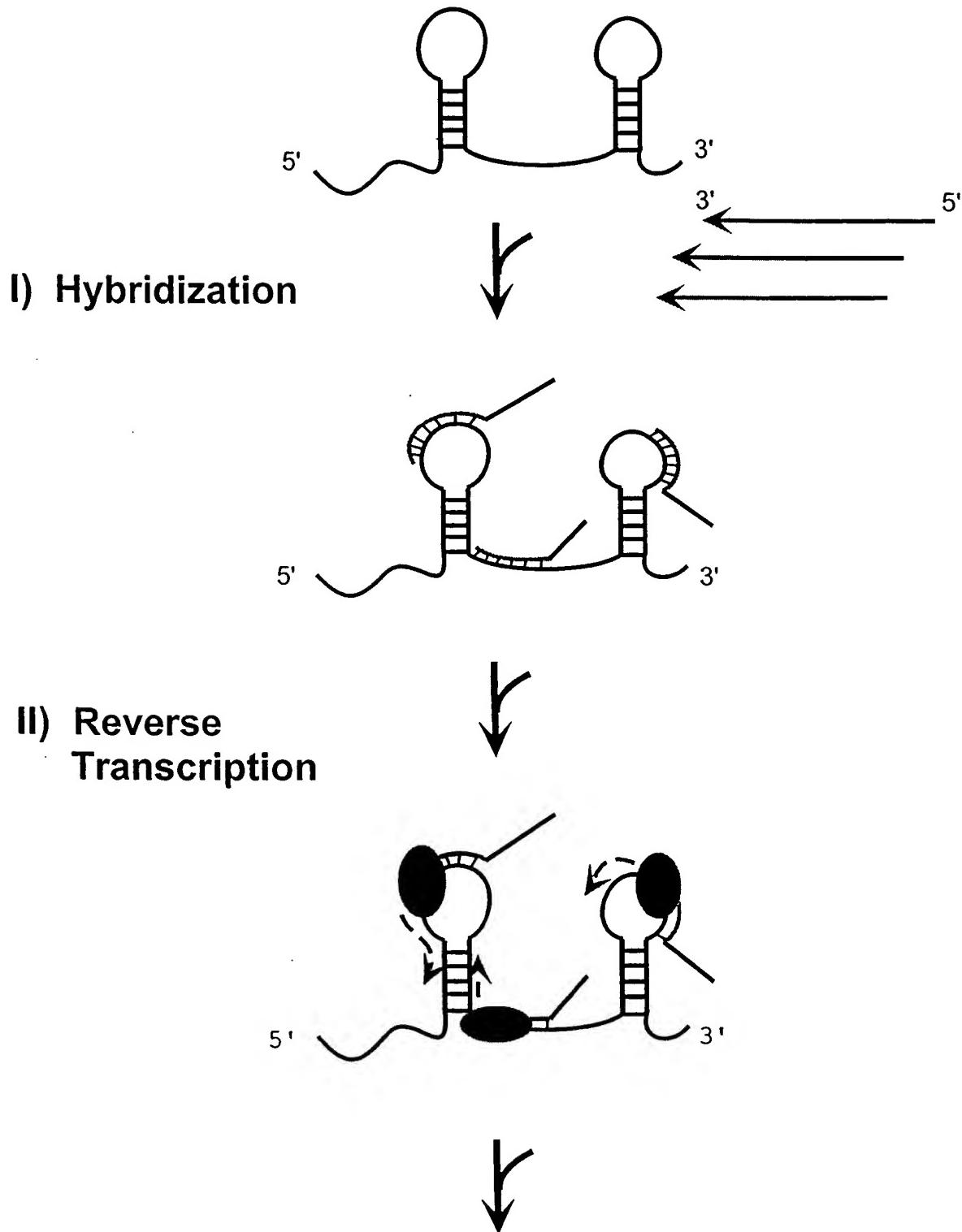
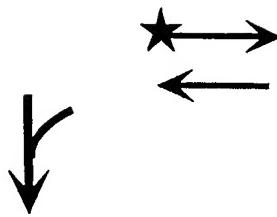
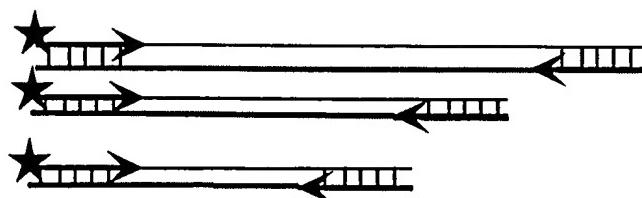


FIGURE 45A



III) PCR



IV) PAGE with Sequencing Ladder

A C G T RT-Products

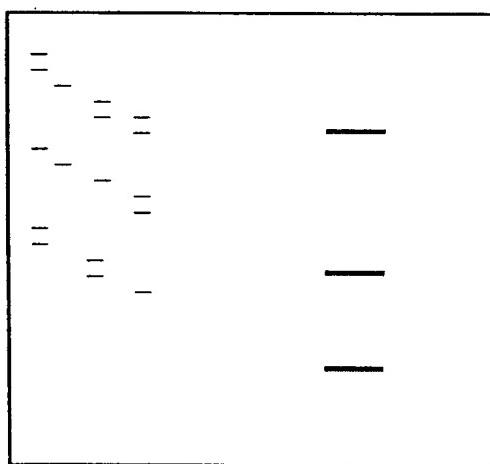
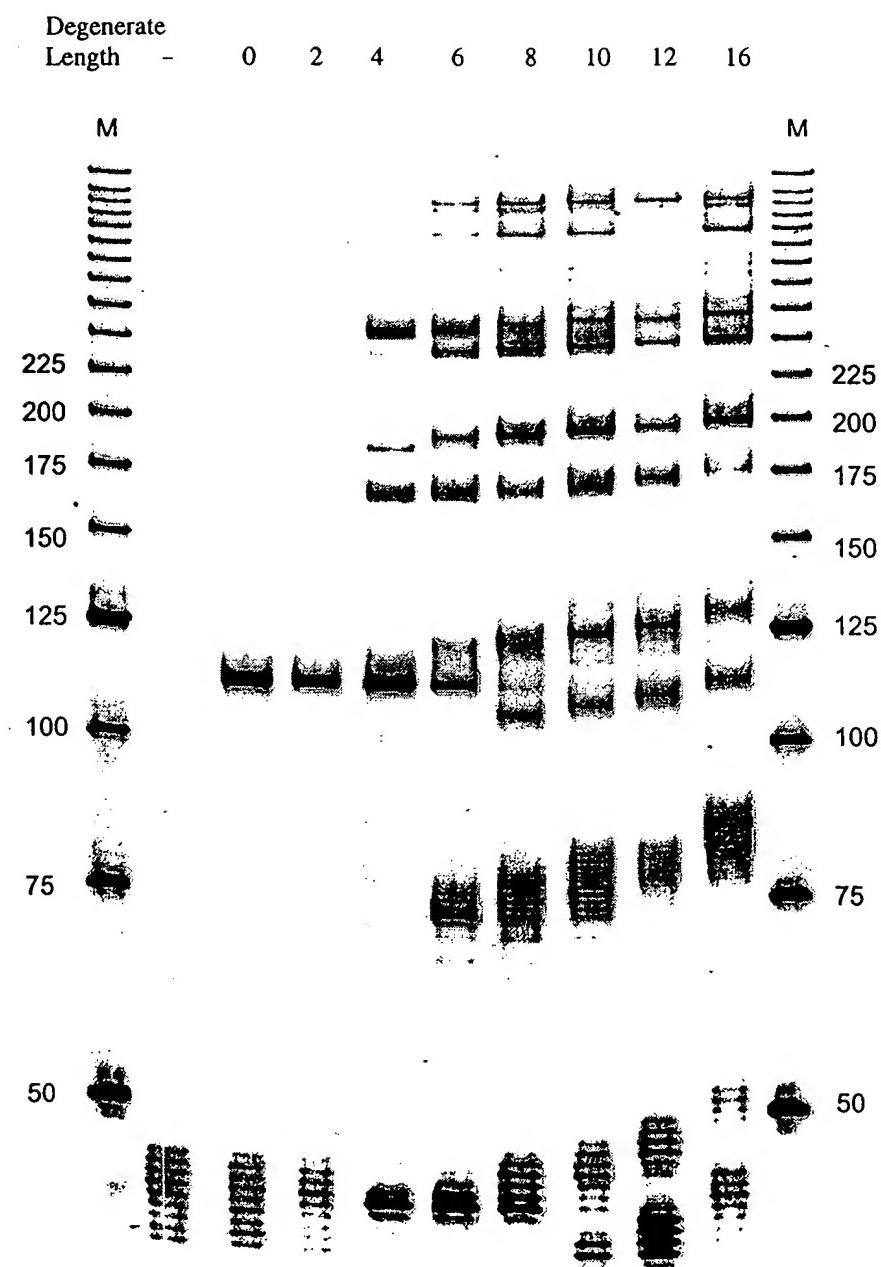


FIGURE 45B

FIGURE 46

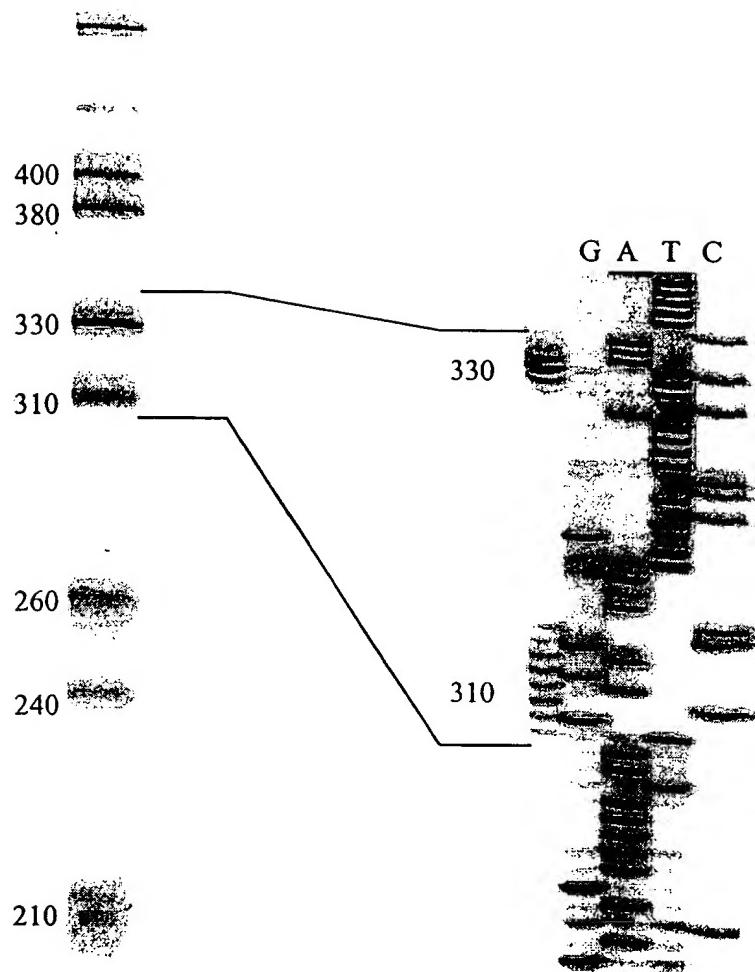


FIGURE 47

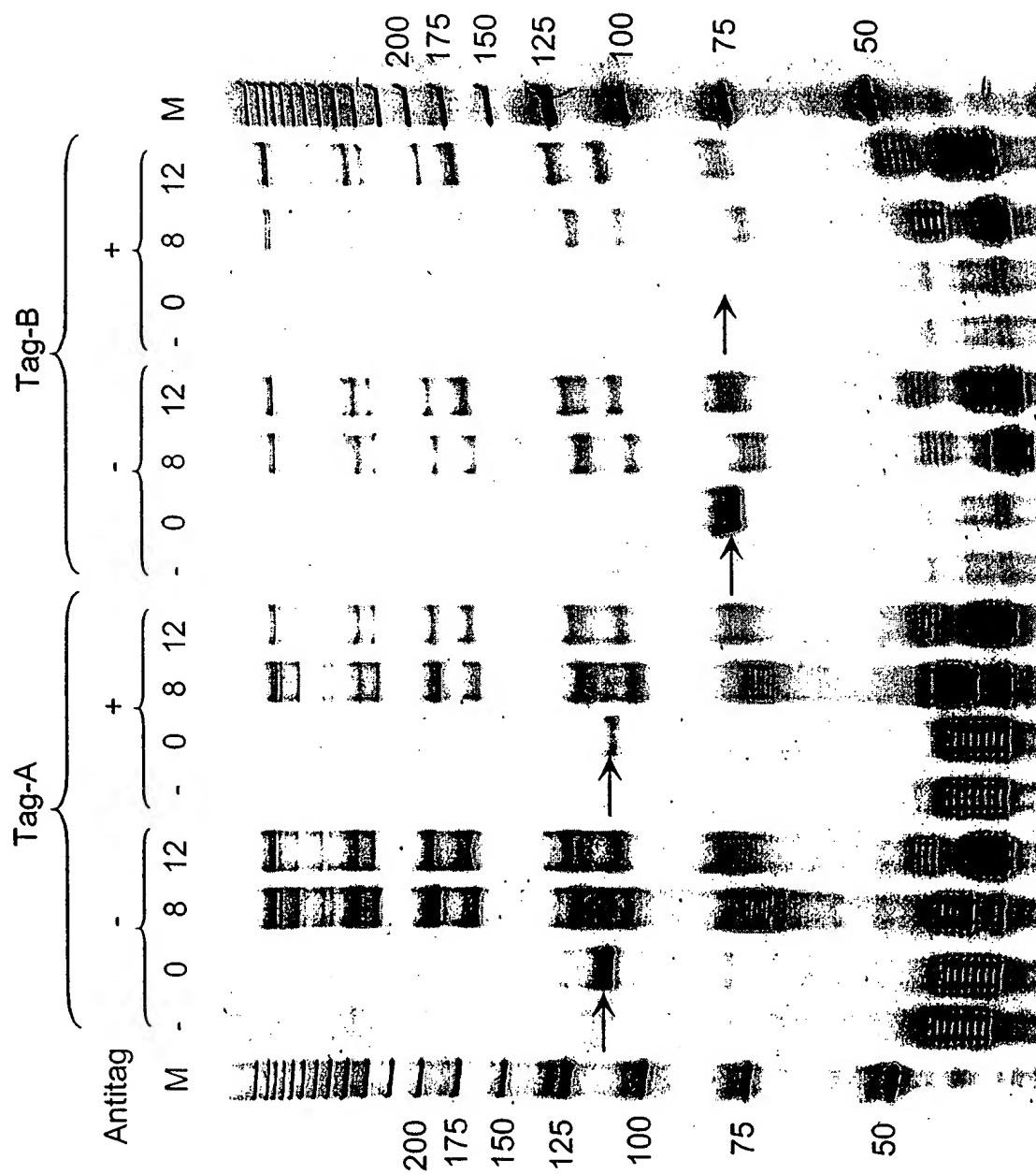


FIGURE 48

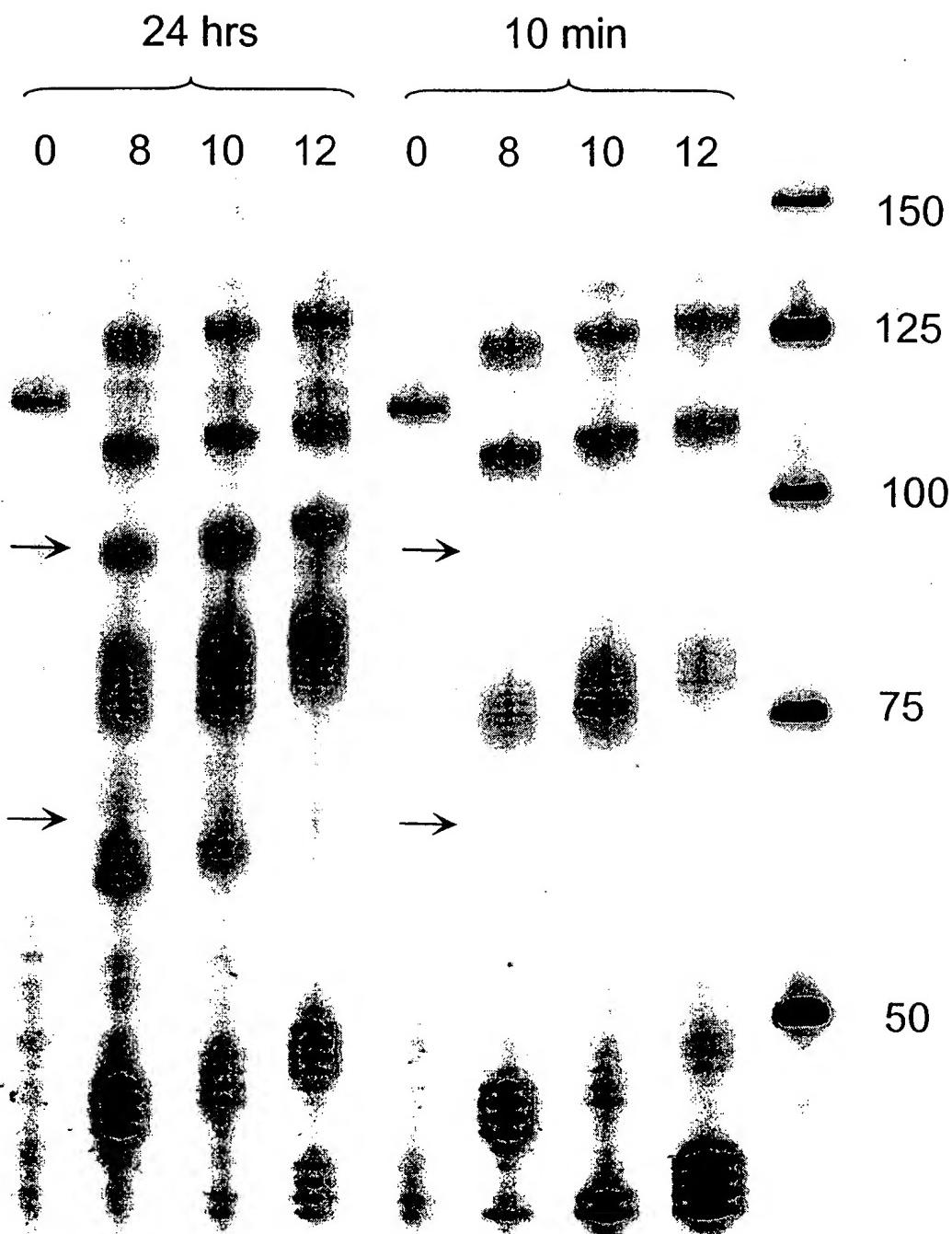


FIGURE 49

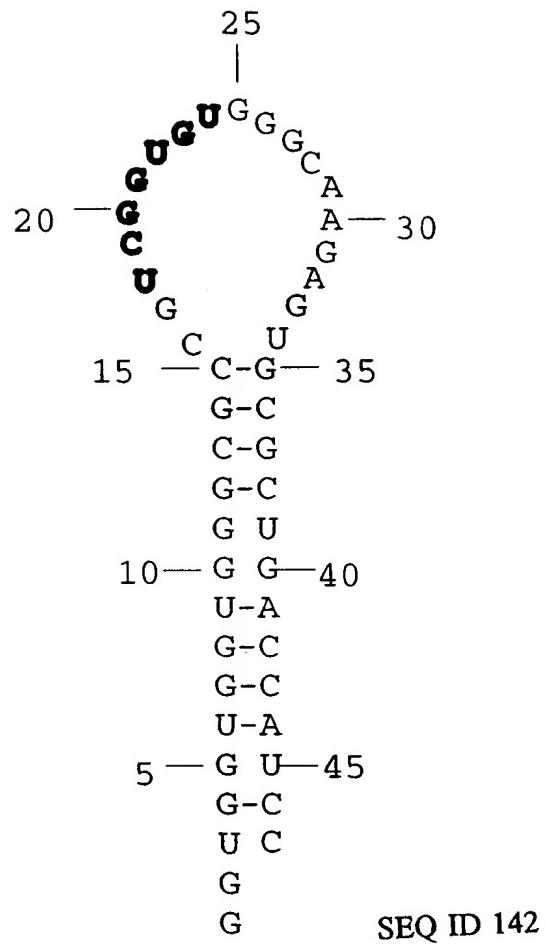


FIGURE 50A

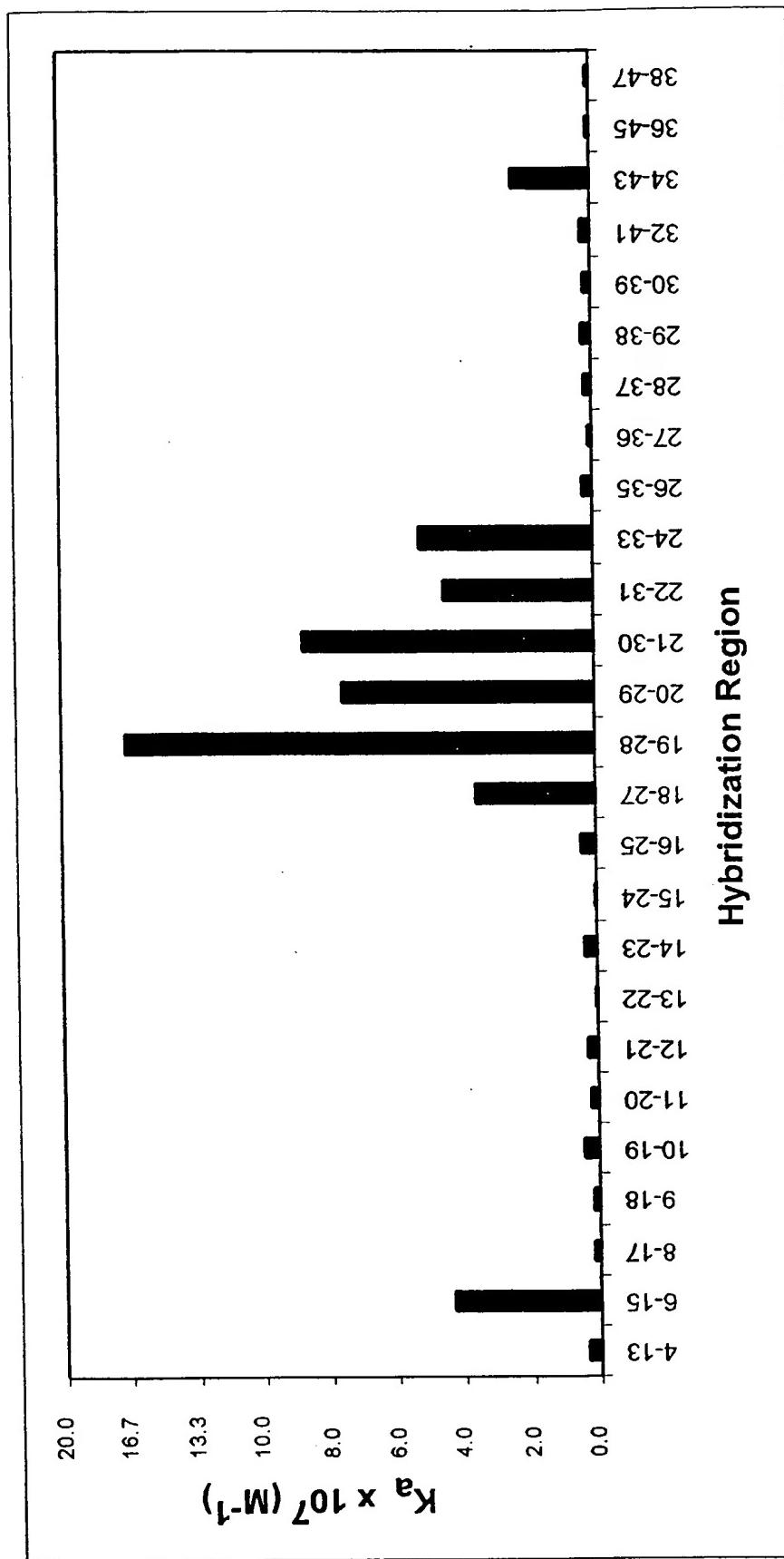


FIGURE 50B

FIGURE 51

44-50

1 ACACUUGC^{UU} UUGACACAAC UGUGUUUACU UGC**AAUCCCC** CAAAACAGAC

64-68 **88-97**

51 AGA**AUGGUGC** AUCUGUCCAG UGAGGAG**AAG** UCUGCGGUCA CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGGUCCUU UGGGGACCUG

FIGURE 52A

ISIS 1571 (-) ISIS 3067 (+)

1 GCGCCCCAGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570 (+)

41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCGGCC81 CGCGCTCCCC GCACTCCCTGG TCCTGCTCGG GGCTCTGTTC121 CCAGGACCTG GCAATGCCCA GACATCTGTG **TCCCCCTCAA**161 AAGTCATCCT GCCCCGGGA GGCTCCGTGC TGGTGACAT**G**201 **CAGCA**CCCTCC TGTGACCAGC CCAAGTTGTT GGGCATAGAG241 **ACCCCGTTGC** CTAAAAAGGA GTTGCTCCTG CCTGGGAACA

281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934 (-)

321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA

361 ACAGCTAAAA CCTTCCTCAC CGTGTACTGG ACTCCAGAAC

401 GGGTGGAACT **GGCACCCCTC** CCCTCTTGGC AGCCAGTGGG441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGG**CA**481 **CCCCGGGCCA** ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA
as 610
561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA

601 GCCAATTCT **CGTGCCGCAC** TGAACTGGAC CTGCGGCC

641 AAGGGCTGGA GCTGTTGAG AACACCTCGG CCCCCTACCA

681 GCTCCAGACC TTTGTCC**TGC** CAGCGACTCC CCCACAACTT

721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG

761 TGGTCTGTT C**C**CTGGACGGG CTGTTCCAG TCTCGGAGGC

801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC

841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT

881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT

921 GACGTGTGCA GTAATACTGG GGAACCAGAG **CCAGGAGACA**

961 CTGCAGACAG **TGACCATCTA** CAGCTTCCG GCGCCAACG

1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

FIGURE 52C

1041 GACAGTGAAG **TGTGAGGCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCC GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTATG

1241 **GCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGCCAGAA AATTCCCAGC **AGACTCCAAT** GTGCCAGGCT

1321 TGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTTTCCC ACTGCCATC GGGGAATCAG TGACTGTCAC

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CTGCAGGCCT **CAGCACGTAC**

FIGURE 52D

1561 CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC

as 1630 as 1630h (+++)

1601 AACAGGCCCA AAAAGGGACC CCCATGAAAC CGAACACACA

ISIS 1938 (+)

1641 AGCCAC GCCT CCCTGAACCT ATCCCAGGAC AGGGCCTCTT

1681 CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCTACCGG

1761 CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 TACAACAGCA TTTGGGGCCA TGGTACCTGC ACACCTAAAA

1841 CACTAGGCCA CGCATCTGAT CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA

1961 CATAGCCCCA CCATGAGGAC ATACAACTGG GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA

2041 CAGAAGAAGT GGCCCTCCAT AGACATGTGT AGCATCAAA

FIGURE 52E

ISIS 2302 (+)
2081 CACAAAGGCC CACACTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA CTGACCCCCAA CCCTTGATGA TATGTATTAA

ISIS 1572
2161 TTCATTTGTT ATTTACCAG CTATTTATTG AGTGTCTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTC TATCGGCACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTTCAGAG ATTACCCAGT

2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT

2481 GTTAGCCACC TCCCCACCA CATACATTC TGCCAGTGT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGAATATG CCCAAAGCTAT GCCTTGTCCCT CTTGTCCCTGT

FIGURE 52F

2601 TTGCATTC CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCCGGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

FIGURE 53A

1 CACAUUGUUC UGAUCAUCUG AAGAUCAGCU AUUAGAAGAG

site 80

41 AAAGAUCAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC

site 120

81 AAAGAACUACU GAUUUCAACU UCUUJGGCUU AAUUCUCUCG

121 GAAACGAUGA AAUAUACAAG UUUAUACUUG GCUUUUCAGC

161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA

site 210

201 CCCAU AUGUA **CAAGAAGCAG** AAAACCUUAA GAAAUAUUUU

site 240

site 260

241 AAUGCAGGGUC AUUCAGAUGU **AGCGGAUAAU** GGAACUCUUU

281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG

site 330

321 AAAAAUAAUG **CAGAGCCAAA** UUGUCUCCUU UUACUUCAA

site 380

site 400

361 CUUUUUAAAA ACUUUAAAGA **UGACCA**GAGC AUCCAAAAGA

401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU

441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

FIGURE 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG
521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC site 560
561 AGCAGCUAAA ACAGGGAAAGC GAAAAAGGAG UCAGAUGCUG site 570
601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC
641 UACAAUAUUU GAAUUUUAAA UCUAAAUCUA UUUAUUAAUA
681 UUUAACAUUA UUUUAUAGGG GAAUUAUUU UUAGACUCAU
721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG
761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUAU UUAUAAUUC
801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA
841 CUAAUUAGGC AAGGCUAUGU GAUUACAAGG CUJUAUCUCA site 850 site 860 site 881
881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG site 890 site 910
921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUAU
961 AAGUGAAGUG AUACUAUCCA GUUACUA

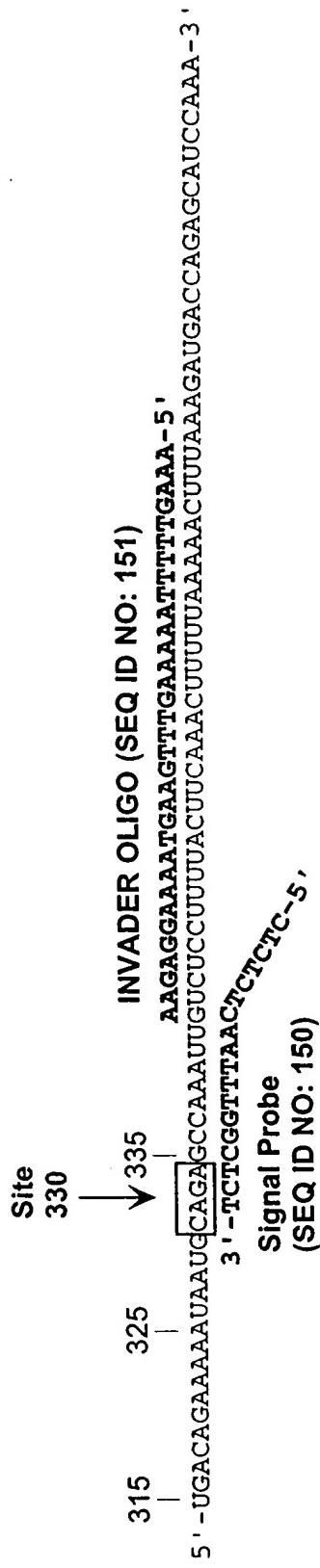


FIGURE 54A

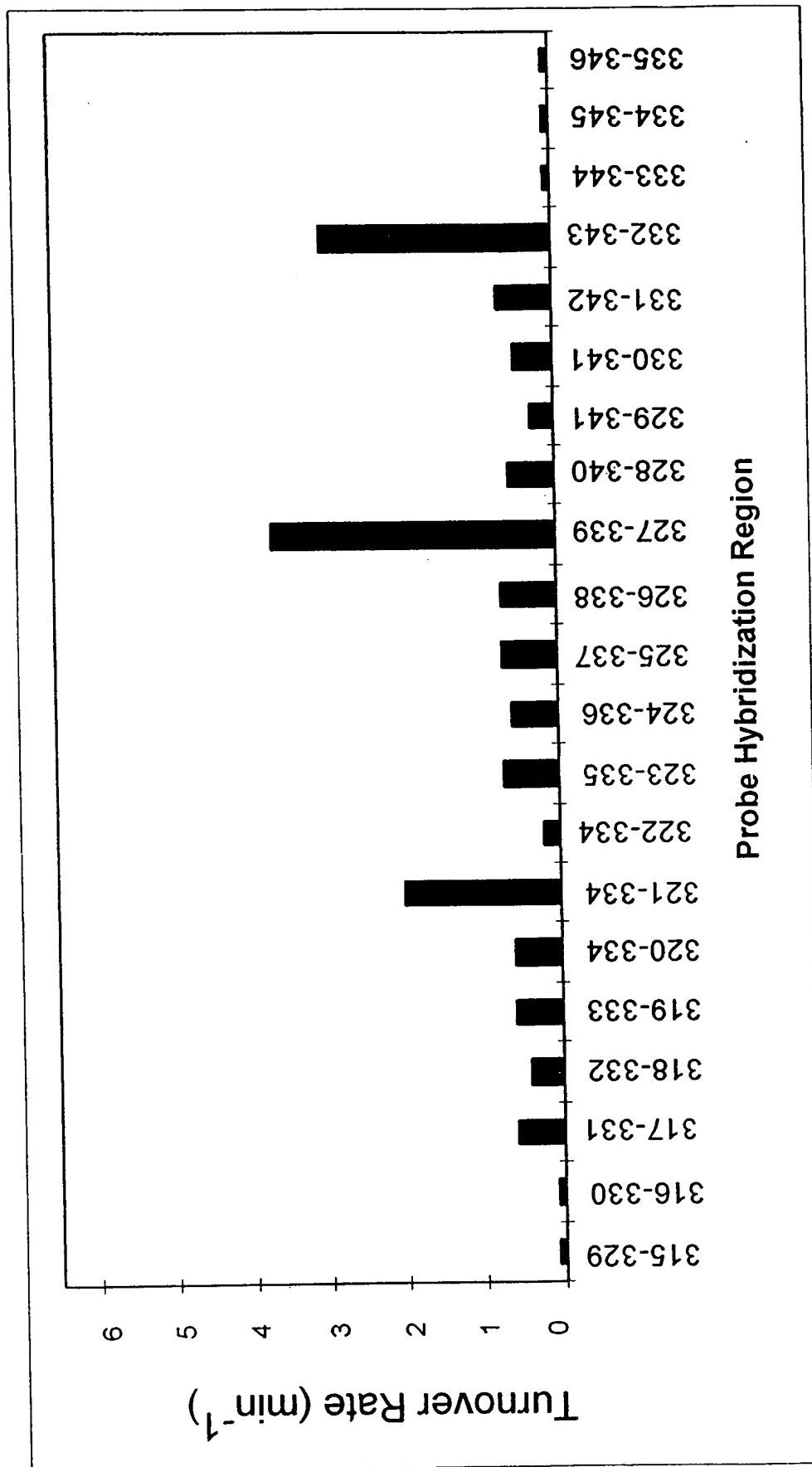


FIGURE 54B

FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUAA CGGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUCAAGAA

960 GGCUGUAGAC AAAUACUGGG ACAGCUACAA CCAUCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUAU AUAAUACAGU AGCAACCCUC UAUUGUGUGC1060 AUCAAAGGAU AGAGAUAAAA GACAC**CCAAGG** AAGCUUUAGA CAAGAUAG**GAG**

FIGURE 55B

1110 **GAA**GAGCAAA ACAAAAGUAA GAAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGG**ACACAGC AAUCAGGUCA GCCAAAAAUUA CCCUAUAGUG CAGAACAUCC

Primer 5

1210 **AGGGGCAAAU** GGUACAU~~CAG~~ GCCAU~~AUCAC~~ CUAGA~~ACUUU~~ AAAUGCAU~~GG~~

1260 GUAAAAGUAG UAGAAGAGAA GGC~~UUUCAGC~~ CCAGAAGUGA UACCCAU~~GUU~~

1310 UUCAGCAUUA UCAGA**AGGAG** **CC**ACCCCCACA AGAUUUAAAC ACCAUGC~~UAA~~

1360 ACACAGUGGG GGGACAUCA **GCA**GCCAUGC AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUGA**GGAAAG CUGCAGAAU GGAU~~AGAGUG~~ CAUCC~~AGUGC~~ AUGCAGGGCC

1460 UAUUGCACCA GGCCAGAUGA GAGA**ACCAAG** GGGAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAAUUA UAAAAGAUGG AUAAUCCUGG GAUAAAUA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAUA AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAA AACUCUAAGA

1710 **GCCGAG**CAAG CUUC**ACAGGA** GGUAAAAAU **UGGA**UGACAG AAACCUUGUU

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGCGGCUAC ACUAGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGGAGGA**

1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUAAUGAUGC **AGAGAGGCAA** UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGA**AG** GGCACACAGC CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

FIGURE 56

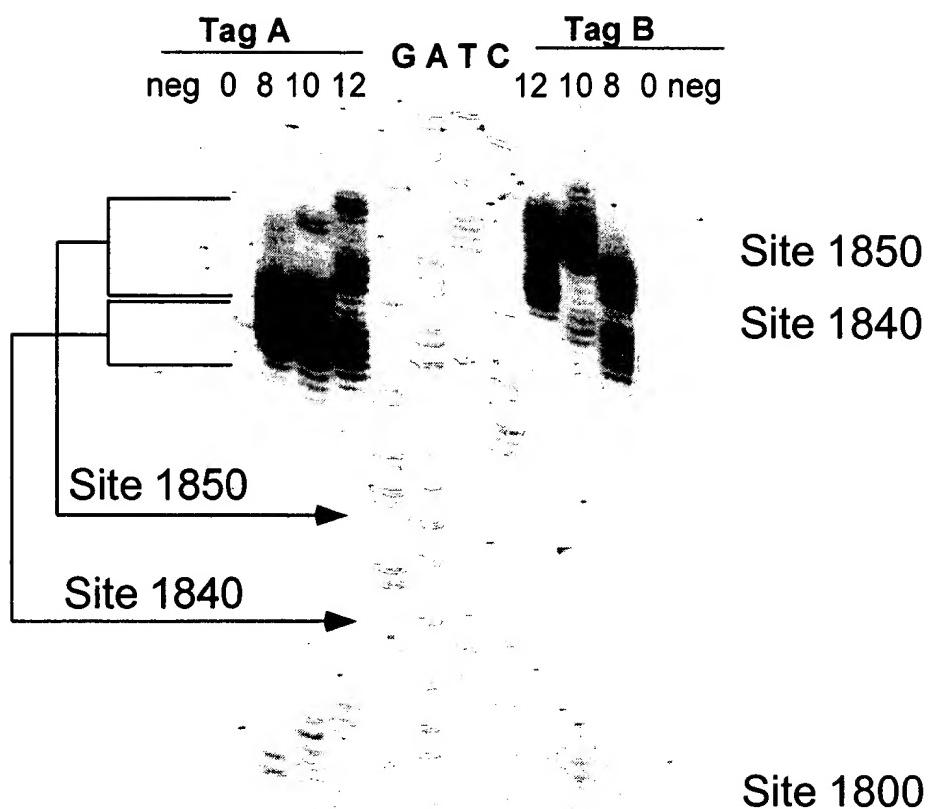


FIGURE 57

(SEQ ID NO: 188)
 (SEQ ID NO: 187)
 (SEQ ID NO: 186)
 (SEQ ID NO: 185)
 (SEQ ID NO: 184)
 (SEQ ID NO: 183)
 (SEQ ID NO: 182)
 (SEQ ID NO: 181)
 (SEQ ID NO: 180)
 (SEQ ID NO: 179)
 (SEQ ID NO: 178)
 (SEQ ID NO: 177)
 5'-CAUGUCAGGGAGGUAGGGACCCGGCCAUAAAGGCAAGAGGUUUGGCUGAAAGCAAUGAG-3'
 1 CAGTCCTCATC
 2 AGTCCCTCATCC
 3 GTCCCTCATCC
 4 TCCCTCATCC
 5 CCCTCATCC
 6 CCTCATCC
 7 CTCCATCC
 8 TCATCC
 9 CATCC
 10 ATCC
 11 TCCTCC
 12 CCTCC
 13 CTCCTCC,
 (SEQ ID NO: 164)
 (SEQ ID NO: 165)
 (SEQ ID NO: 166)
 (SEQ ID NO: 167)
 (SEQ ID NO: 168)
 (SEQ ID NO: 169)
 (SEQ ID NO: 170)
 (SEQ ID NO: 171)
 (SEQ ID NO: 172)
 (SEQ ID NO: 173)
 (SEQ ID NO: 174)
 (SEQ ID NO: 175)
 (SEQ ID NO: 176)

CGTATTCCGGTCTCAAAACCGACTTGCT-5' 13
 AGGTATTCCGGTCTCAAAACCGACT 12
 ACGGTATTCCGGTCTCAAAACCGAC 10=11
 CCCGGTATTCCGGTCTCAAAACCGA 9
 CGCCGGTATTCCGGTCTCAAAACCG 8
 CGGGGGTATTCCGGTCTCAAAAC 7
 AGGGGGTATTCCGGTCTCAAAAC 6
 ATGGGGGGTATTCCGGTCTCAAAA 5
 ACTGGGGGGTATTCCGGTCTCAAA 4
 ACCTGGGGGGTATTCCGGTCTCAAA 3
 ATCCTGGGGGGTATTCCGGTCTCA 2
 ACTCCTGGGGGGTATTCCGGTCTC 1
 (SEQ ID NO: 158)

FIGURE 58

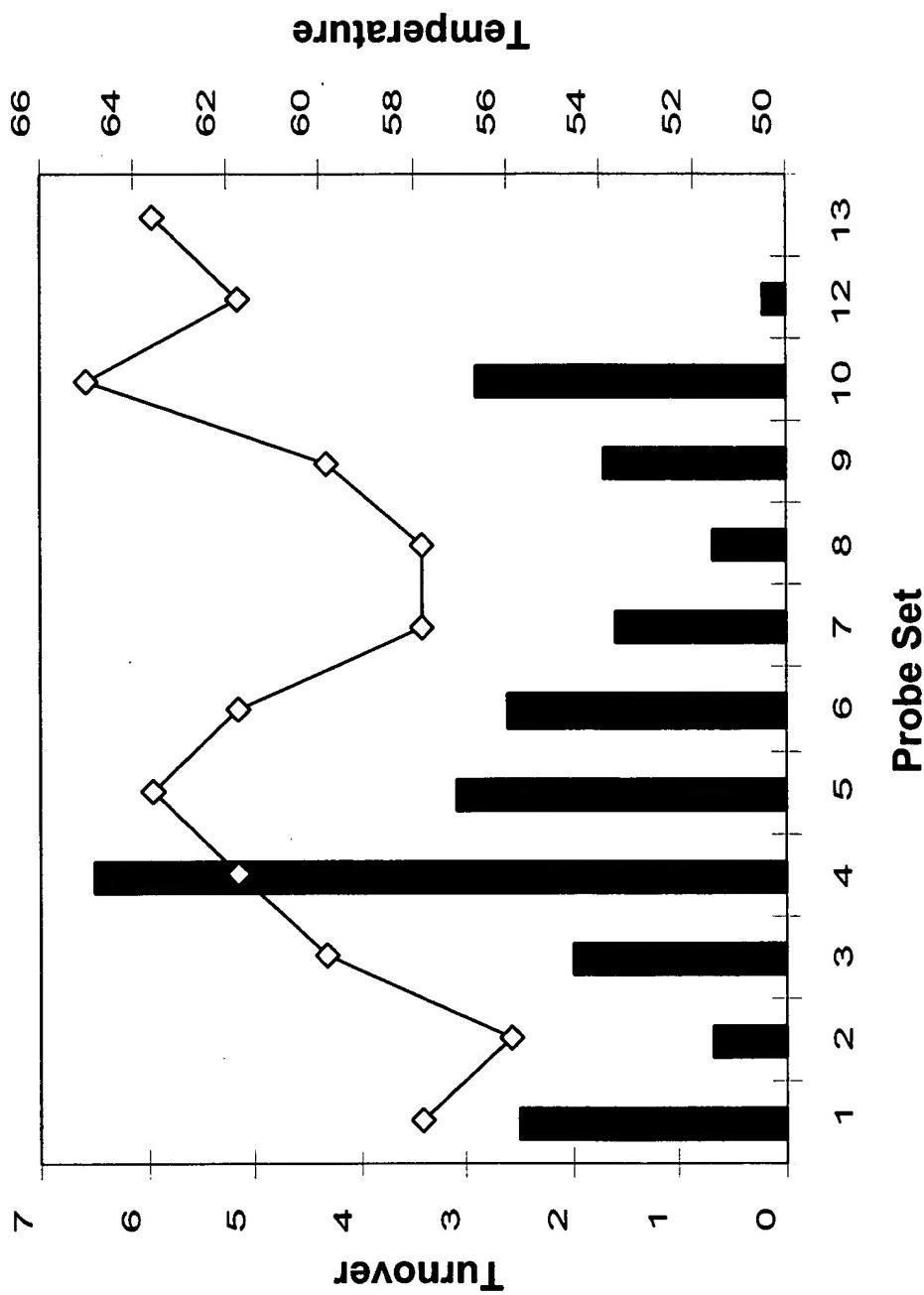


FIGURE 59

5' - CAUGUDGGAGGGUAGGCGGTATTCCGTTCCTCAA
 (SEQ ID NO: 180)

ACTGGGCCGGTATTCCGTTCCTCAA
 TCCCTCATCCTCCTCCGGCACTGCC-_{5'}
 (SEQ ID NO: 158)

(SEQ ID NO: 189) ↑

5' - AGGGACTAGGAGGAGG-3'
(SEQ ID NO: 190)



 (SEQ ID NO: 191)

5' - CCGTCACGCCCTCC

3' - **T**GGCAGTGGGAGGGTTGACGAAG**A**GGC-5'

(SEQ ID NO: 193)

(SEQ ID NO: 192)

FIGURE 60

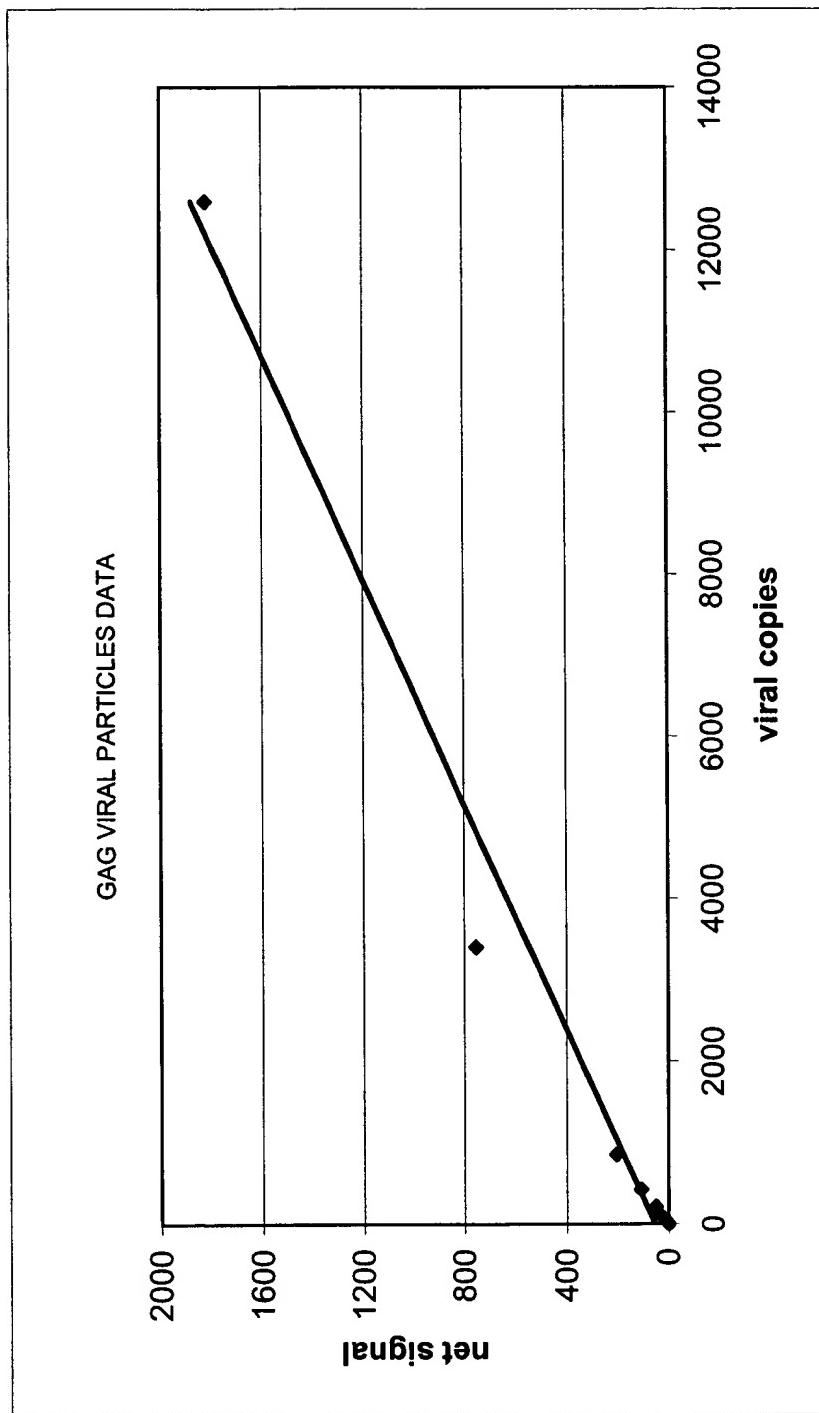


FIGURE 61A

SEQ ID NO:159

primer 1

3300 AGCUGGACUG UCAAUGACAU ACAGAAG**UUA** GUGGGGAAAU UGAAUUGGGC

3350 AAGUCAGAUU **UACCCAGGGA** UUA**AAGUAAG** GCAUUUAUGU AAACUCCUUA

3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG

3450 CUAGAAC**UGG** CAGAAAACAG AGAGAUUCUA AAAGAAC**CCAG** UACAUGGAGU

primer 2

3500 GUAUU AUGAC **CCAUCAAAAG** ACUUAAUAGC AGAAAU**ACAG** **AAGCAGGGGC**

3550 **AAGGCCAAUG** GACAUAUCAA AUUUAU**CAAG** AGCCAUUUAA AAAUCUGAAA

3600 ACAGGAAAAU AUGCAAGAAU **GAGGGGUGCC** CACACUAUAG AUGUAAAACA

3650 AUUAAC**GAG** **GCAGUGCAA** AAAUAACCAC AGAAAGCAUA GUAAUAUGGG

primer 3

3700 GAAAGACUCC UAAAUUUAA CUGCCAUAC AAAAGGAAAC AUGGGAAACA

3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU

3800 UAAUACCCU CCCUUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA

3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGA**UG** **GGGCAGCUAA** **CAGGGAGACU**

primer 4

3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

FIGURE 61B

3950 CACCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC

4000 UAGCUUUGCA GGAAUCGGGA UUAGAAGUAA ACAUAGUAAC AGACUCACAA

4050 UAUGCAAUAG GAAUCAAUCA **AGCACAAACCA** GAUCAAAGUG AAUCAGAGUU

primer 5

4100 AGCUAAUCAA AUAAUAGAGC AGUUAUAAA AAAGGAAAAG GUCUAUCUGG

4150 CAUGGGUACC AGCACACAAA **GGAUUGGAG** GAAAUGAACA AGUAGAUAAA

4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGAUAA

4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAUUGGGAGA GCAAUGGCUA

primer 6

4300 GUGAUUUUAA CCUGCACCU GUAGUAGCAA AAGAAAAGU **AGCCAGCUGU**

4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG

4400 UCCAGGAAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC

4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUA **UAGAA**GCAGA AGUUAUUCCA

primer 7

4500 GCAGAACAG GGCAGGAAAC AGCAUAAAAU CUUUAAAAAU **UAGCAGGAAG**

4550 **AUGGCCAGUA** AAAACAAUAC AUACUGACAA **UGGCAGCAAU** UUCACCGGUG

4600 CUACGGUUAG GGCGGCCUGU UGGUGGGCGG GAAUCA**AGCA** GGAAUUUGGA

FIGURE 61C

4650 AUUCCUACA AUCCCCAAAG UC**AAGGAGUA** GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAGGAC **AGGUAGAGA** **UCAGGCUGAA** CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG **AAAAGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAAAGAAUA** GUAGACAUAA UAGCACACAGA

4850 CAUACAAACU AAAGAAUUAC AAAAACAAAU UACAAAAAUU CAAAAUUUUC

primer 9

4900 GGGUUUAUUA **CAGGGACAGC** AGAAAUCAC UUUGGA**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGAUA AUAGUGACAU

5000 AAAAG**UAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

FIGURE 62

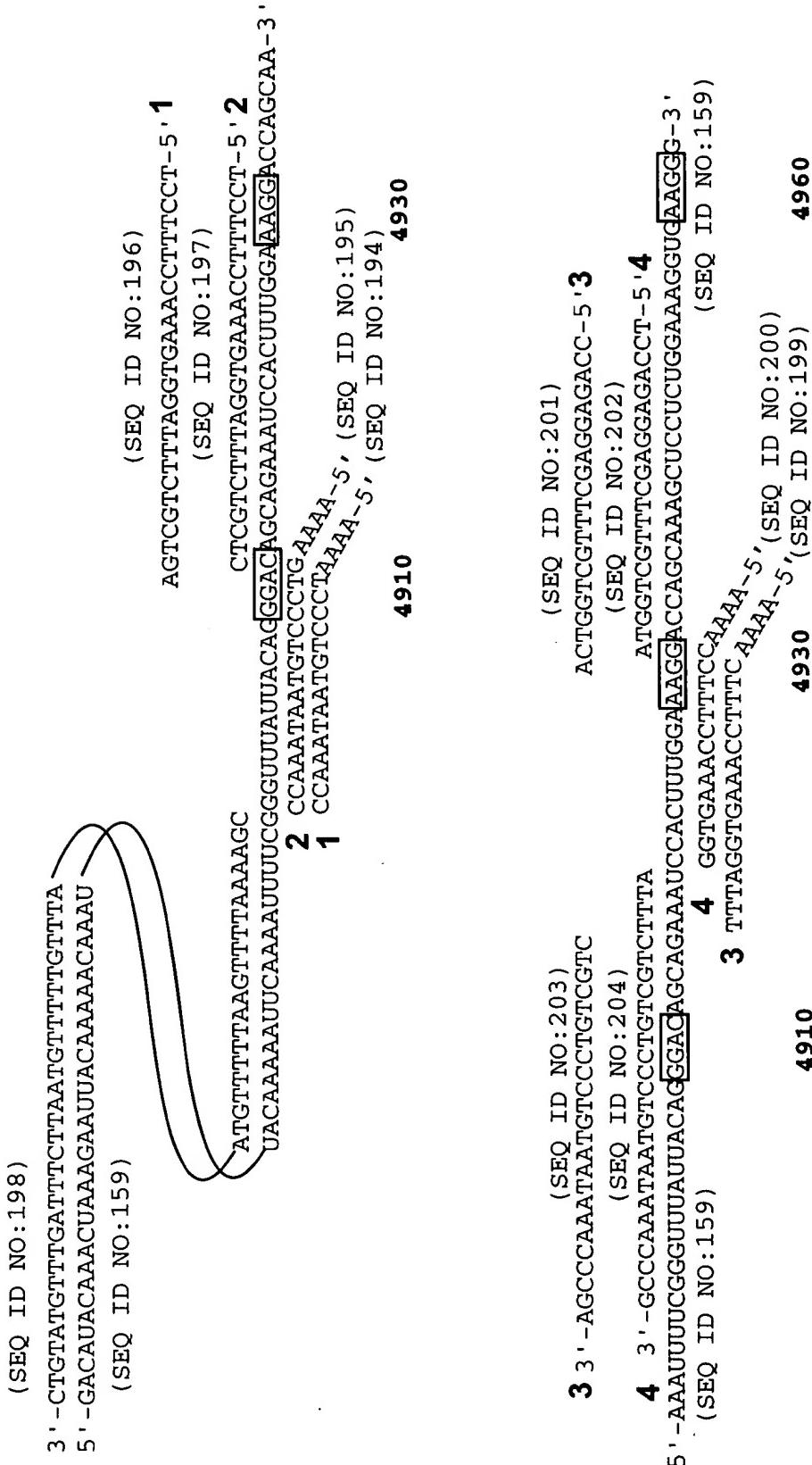


FIGURE 63

5 3' -TCCTGGTTCGAGGA
 (SEQ ID NO: 213)
 ACCCGTCATCATTTACTGTATTTCACGGG-5'
 (SEQ ID NO: 209)

6 3' -CCTGGTTCGAGGA
 (SEQ ID NO: 214)
 ACCGTCACTTATGTTCTATTACTGTATTTCACGGG-5'
 5' -GAAAGGACCAGCAAAGCUCCUCUGGAAAGGU
 6 CTTTCCACTTCCAAAA
 5 CTTTCCACTTCCAAAA
4930 4960 5' (SEQ ID NO: 205)
 (SEQ ID NO: 206)

7 3' -TCGAGGAGACCTTTCCAC
 (SEQ ID NO: 215)
 CTCATTATGTTCTATTACTGTATTTCATCACGG-5'
 (SEQ ID NO: 211)

8 3' -TCGAGGAGACCTTTCCACT
 5' -GAAAGGACCAGCAAAGCUCCUCUGGAAAGGU
 8 TCCCCGTCAAAA
4930 7 4960 5' (SEQ ID NO: 207)
 (SEQ ID NO: 208)

6 3' -CCTGGTTCGAGGA
 (SEQ ID NO: 210)
 ACCGTCACTTATGTTCTATTACTGTATTTCACGGG-5'
 5' -GAAAGGACCAGCAAAGCUCCUCUGGAAAGGU
 6 CTTTCCACTTCCAAAA
 (SEQ ID NO: 159) 5000

7 3' -TCGAGGAGACCTTTCCAC
 (SEQ ID NO: 216)
 ACATTATGTTCTATTACTGTATTTCATCACGG-5'
 (SEQ ID NO: 212)

8 3' -TCGAGGAGACCTTTCCACT
 5' -GAAAGGACCAGCAAAGCUCCUCUGGAAAGGU
 8 TCCCCGTCAAAA
4930 7 4960 5' (SEQ ID NO: 208)
 (SEQ ID NO: 207)

6 3' -CCTGGTTCGAGGA
 (SEQ ID NO: 210)
 ACCGTCACTTATGTTCTATTACTGTATTTCACGGG-5'
 5' -GAAAGGACCAGCAAAGCUCCUCUGGAAAGGU
 6 CTTTCCACTTCCAAAA
 (SEQ ID NO: 159) 5000

FIGURE 64

1	4790	4810
	(SEQ ID NO:224)	(SEQ ID NO:221)
	3' - TCCCCCTAACCCCCCATG 5' - AAGAA <u>AGGGGGGAU</u> GGCAACAUAAUAGCAA <u>ACAGACAU</u> AACU-3'	ATTTCTTATTCTGTATTATCGTTGTC <u>TGTATG</u> T-5' <u>AGUGCAGGGAA</u> AGAAAUAGCAACAUAAUAGCAA <u>ACAGACAU</u> AACU-3' TCACGTCCCC <u>AAAAA</u> -5', (SEQ ID NO:217)
		(SEQ ID NO:159)

2, 4	4790	4810
	(SEQ ID NO: 225)	(SEQ ID NO: 222)
3' -CTGTCGTACGGTACATGTTAACGTATAAGTAGGT 5' -AGACAGCAGUACAAUGGCAGGUAUUCACAAUAAAAGAAAGGGGGAUUGGGGUACAGUGCAGGGGA	ACCCCTAACCCCCCATGTCAC-5' GTTAAAATTTCCTTTCCC ^T ATATA	AAG-3' (SEQ ID NO: 159)
	GTTAAAATTTCCTTTCCC ^A AAA-5'	(SEQ ID NO: 220)
		(SEQ ID NO: 218)

4790	4810	
3	(SEQ ID NO: 222)	(SEQ ID NO: 223)
	ACCCTAACCCCCCATGTAC-5'	CATCATCTGTATTATGTTGTCGTATGTTGATTTC
	5' - AAA <u>AGGGGGCAUUGGGGUAD</u> <u>AGGGCAGGGAA</u> AGAAAUAGUAGACAUAAUAGCAAACAGACAUAAACUAAGAAA-3'	GTCGCCCTTCTTA <u>AAAA</u> -5' (SEQ ID NO: 159)

FIGURE 65

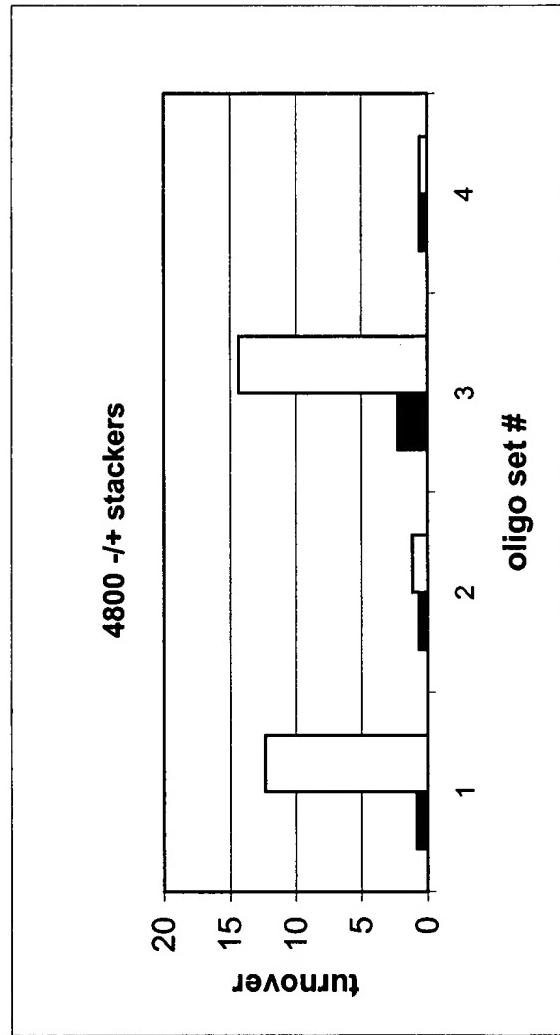


FIGURE 66

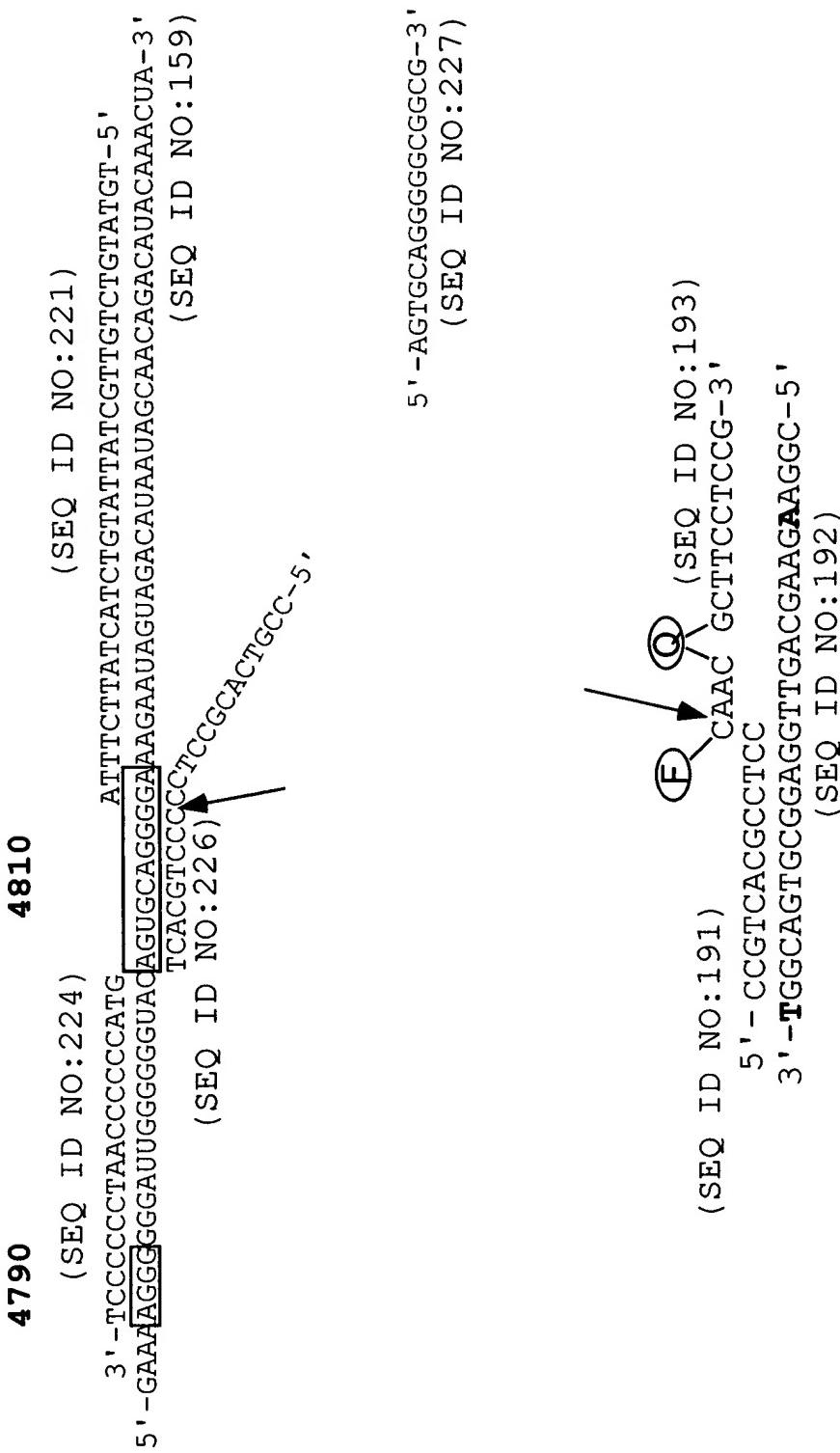


FIGURE 67

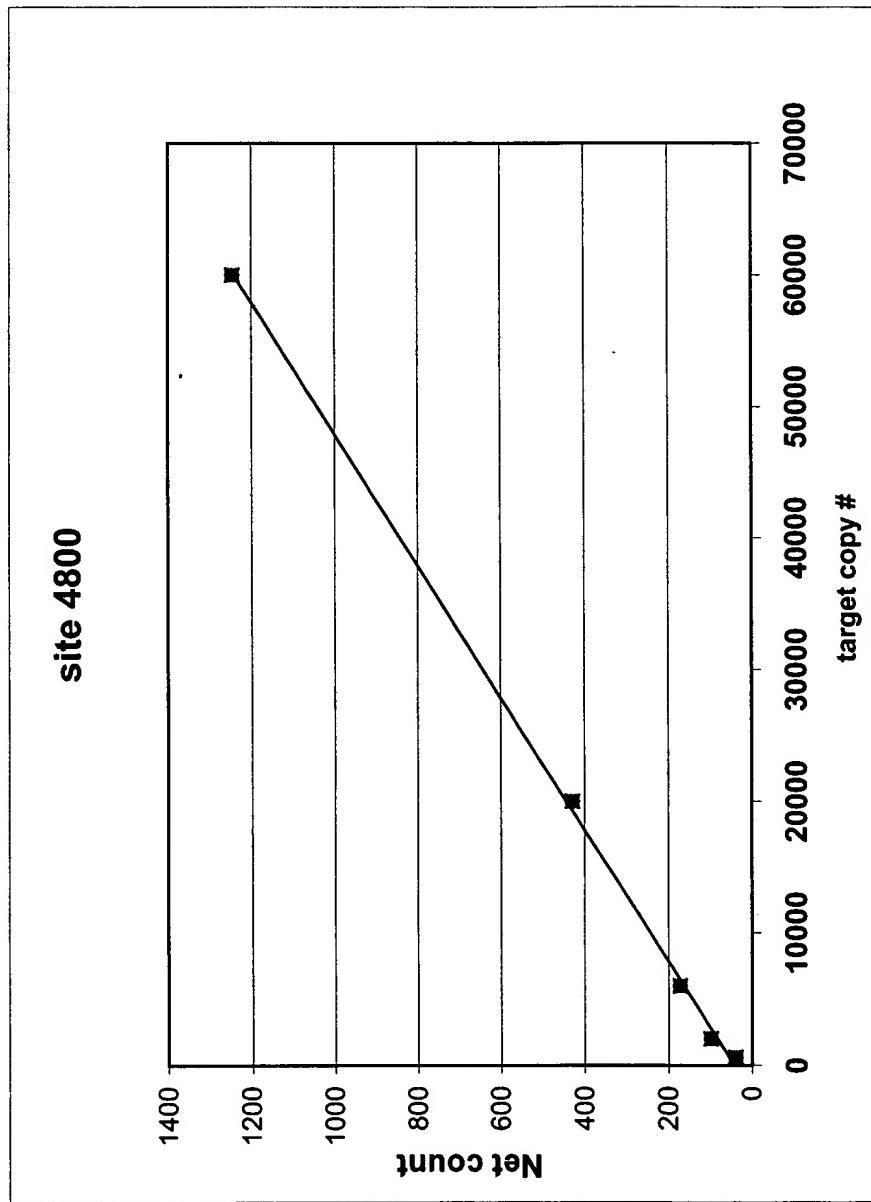


FIGURE 68

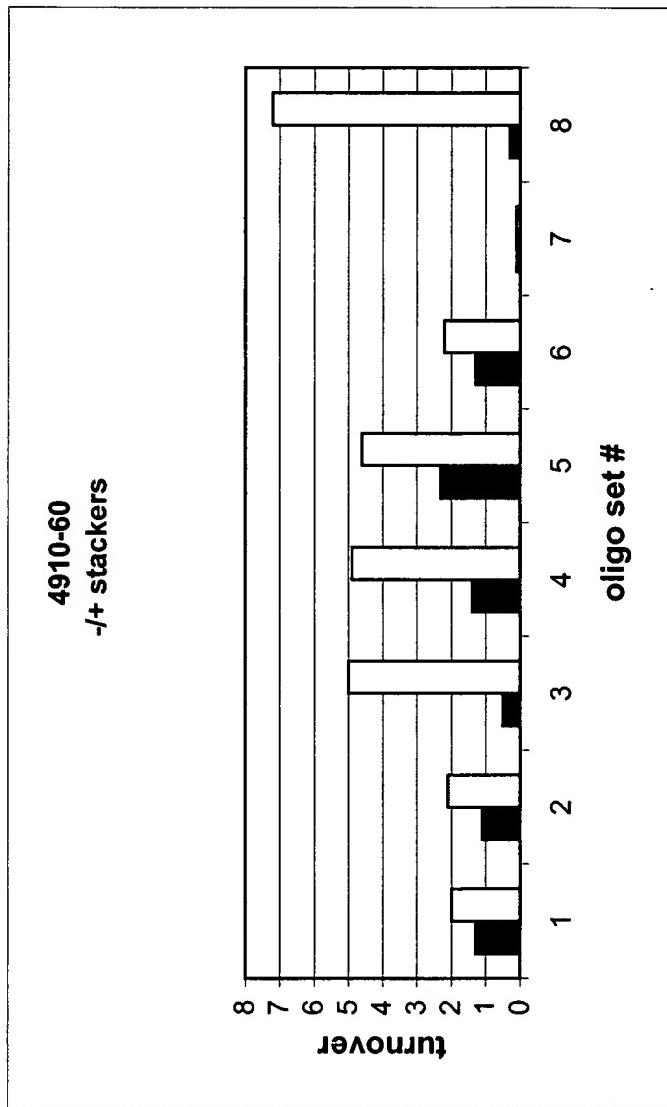


FIGURE 69

(SEQ ID NO: 213) 4960 (SEQ ID NO: 209)
 3' - TCCCTGGTCGTTCGAGGAGA
 5' - GAAAGGACCAGCAAAGCUCCUCUGGAAAGGUGAAGGGGCAGUAGUAUACAAGAUAAGUAGGC-3'
 (SEQ ID NO: 159) 5000

4930 (SEQ ID NO: 228) CTTTCCACTTCCTCCGCACTGCC-5,

5' - GGAAAGGTGAAGGAGGC-3'
 (SEQ ID NO: 229)

(SEQ ID NO: 191) F Q (SEQ ID NO: 193)
 5' - CCGTCACGCCTCC
 3' - **T**GGCAGTGCGGAGGTGACGAAGAGGC-5'
 (SEQ ID NO: 192)

FIGURE 70

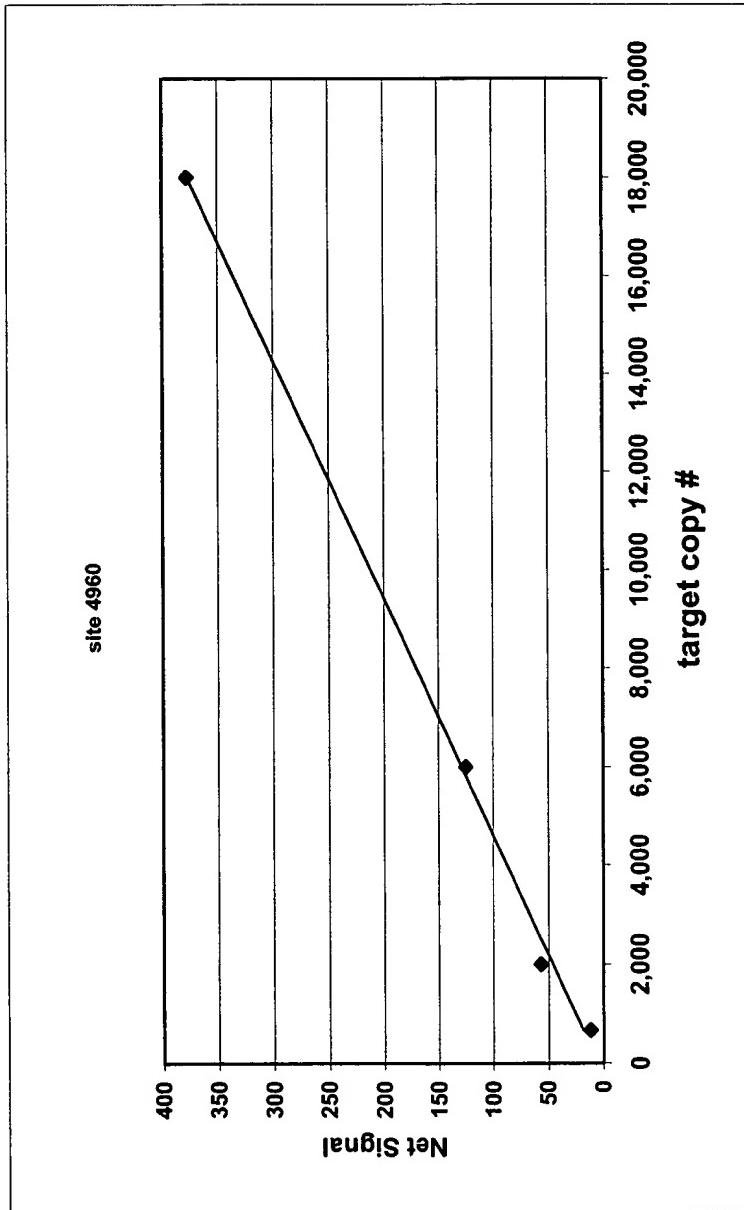


FIGURE 71**Human PSP94**

383-31-1 5'-TET-CCTGCTTATCACAAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGG **GCAGCGUUG** UGAUCUUUGCACCUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUCAUACCUAAUGAGGGAGUCCAGGAGAUUCAACCA
GGAAAUGCAUGGAUCUAAAGGAAACAAACACCCAAUAAACUCGG **AGUGG** CAGACUGAC
AACUGUG **AGACAUG** CAC **UUGC** UACGAAACAGAAAUUUCAUGUU **GCACC** CUUGUUUCUAC
ACCUGUG GGUUAUGACA **AAGACA** ACUGCCAAAGAAUC **UUCAAGAAGGAGGA** CUGCAAGU
AUAUCG **UGGUGGAGAAGAAGGACC** CAAAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUCCCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA
AUAGUCAAUGAUUGUGUAGCCAUGCCUAUCAGUAAAAGAUUUUUG

FIGURE 72**Human ubiquitin:**

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)
520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235
CCGCCACCAAAUGCAGAUUUUCGUGAAAACCUUACGGGGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUAAAGGCCAAGAUCCAGGAUAAGGAAGGAAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUUAUCAAAAGGAGUCUACUCUUCAUCUUGUGUUGAGACUUCGUGGUGG
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAGCUGGCUGGUCCUGAAAUAUUAAGGUGGAUGAGAAUGGCAAAAUUAGUC
GCCUUCGUCGAGAGUGCCCUCUGAUGAAUGUGGUGCUGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA

FIGURE 73**HCV-1a 5'-UTR:**

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUGUCGUGCAGCCUCCAGGACCCCCCCUCCGGGAGAG
CCAUAGUGGUUCUGCGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUAAACCCGCUCAUGCGAUGCUAGCC
AGUAGUGUUGGGUCGGAAGGCUUGGUGC
CCGGGAGGUCUGUAGACCGUGCACCAUGAG

FIGURE 74**HCV-1b 5' -UTR:**

898-28-02 5' -TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5' -TET-CGGGAGAGCCATAGTGGTCTGC GG-3' (SEQ ID NO:237)
898-35-02 5' -TET-ATTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5' -TET-GACCGGGTCCTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG
CCAUAGUGGUUCUGCGGAACCGGUGAGUACACCGGAAUUGCAGGACGACCGGGGUCCUUUC
UUGGAUCAACCCGUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGCGAGACUGCUAGCCG
AGUAGUGUUGGGUCGC GAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)

898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)

898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)

898-35-03 5'-TET-GACCGGGTCCTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCUCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGG[CCCCCC]UC[CCG]GGAGAG
CCAUAGUGGUUCUGCGAACCGGUGAGUACACCGGAAUUGCCGGGAAGACUGGGUCCUUUC
UUGGAUAAACCCACCUAUGCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCAGAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUGUAGACCGU[GCACCAUGAG]

FIGURE 76

HCV 3a 5' -UTR:

898-28-03 5' -TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5' -TET-CGGGAGAGCCATAGTGGTCTGC GG-3' (SEQ ID NO:237)
898-35-02 5' -TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5' -TET-GACCGGGTCTTCCTTGGGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGCUUCAGCGGAAAGCGC
CUAGCCAUGGCCUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUCCGGAGAG
CCAUAGUGGUUCUGCGAACCGGUGAGUACACCGGAAUCGCUGGGUGACCGGGUCCUUUC
UUGGAACAACCCGUCAAUACCCAGAAAUUGGGCGUGCCCCCGCGAGAUCACUAGCCG
AGUAGUGUUGGGUCGC GAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCAGUGCC
CCGGGAGGUCUGUAGACCGUGCACCAUGAG

FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aaggaaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgc当地aaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtc当地gg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagtttggatcttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caataactgc当地atggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgttctgc当地aga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAUCAAUCCAGGA
GUUUGCAAGAACAGGUGCUUACACUAAUCACCUCCGAACAAGAAAAAUGGGCUGU
GACCGGAACCUGUGGGCUCAUCGCUGGGGCUGUCAUUGGUGCUGUCCUGGCUGGUUUGG
AGGUAAUCUAAGCCAGUGGGAGACCUGCUUAUCCGAAGACAAUAAAAAGCAAGUUG
UCCUCGAAGAAGGUACAAUUGCUUUAAAUUGGUAAACAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUJUGAUGUGCAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUUUCCUGCAGCCCAAUGGUGCCAUC
UUCGAACCUUACACUACAGUJUGGAACAGAGGCUGACAACUUCACAGUUCUAAUCUGGC
UGUGGCAGCUGCAUCCAAUUCUAUCAAAUCAUUUGUUCAAAUGAUCCUAAUUCAC
UUAAUUAACAAGUAAAUCUUCUAUGUUCCAGUCAGAACUUUGAGAGAACUGUUAUGG
GGCUAUAGGAUCCAUUUJUGAGUUJUGGUCCGUACCCUGUUACUACAGUJUGGUUC
UUUAUCCUUACAACAAAUCUGCAGAUGGAGUUUAAGUUUCAUGAAAAGAUAA
CAUAAGUAAAGUUGCCAAAAUCGACACAUUAAGGUAAAAGGAAUCUGUCCUAAUGGG
AAAGUCACUGCGACAUGAUUAUGGUACAGAUGCAGCCCUAUUCCACCUUJUGAG
AAAAGCCAGGUAUUGCAGUUCUUUCUGAUJUGCAGGUCAUCUAUGCUGUAUU
UGAAUCCGACGUAAUCUGAAAGGAAUCCCUGUGUAAGAUUCGUUCUCCUCCAAGG
CCUUUGCCUCUCCAGUUGAAACCCGACAACUAIUGUUUCUGCACAGAAAAAAUUAUC
UCAAAAAAUUGUACAUCAUAUGGUGUGCUAGACAUCAGCAAAUGCAAAGAAGGGAGACC
UGUGUACAUUCACUCCUCAUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAACCAAAUGAAGAAGAACAUAGGACAUACUUGGAUUAUCAACCUAUAACUG
GAUUCACUUUACAAUJGCAAACGGCUGCAGGGUCAACCUUJGGUCAAGCCAUCAGAA
AAAUUCAAGUAAUAAAAGAAUCUGAAGAGGAACUAAUJUGUGCCUAAUJCUUJGGCUUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCCAA

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01	5' -ATGGGGTTTGTAAAGTTG-3'	(SEQ ID NO:260)
761-47-02	5' -GCTGGGTTAGCTCTCAGCAGCCGC-3'	(SEQ ID NO:261)
937-05-01	5' -TET- atggggtttgttaaagtt-3'	(SEQ ID NO:262)
937-05-02	5' -TET- gaagacgacgagagg-3'	(SEQ ID NO:263)
937-05-03	5' -TET- ggatgatagttcgtgt-3'	(SEQ ID NO:264)
937-05-04	5' -TET- gctgcagcatattgt-3'	(SEQ ID NO:265)
937-05-05	5' -TET- ctgctattggatgca-3'	(SEQ ID NO:266)
937-05-06	5' -TET- gcagaagtacatcgga-3'	(SEQ ID NO:267)
937-05-07	5' -TET- gacatgatggaggaga-3'	(SEQ ID NO:268)
937-05-08	5' -TET- agaagaaggatcggg-3'	(SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAAGUUGUUAAGAAUAAGGCCUACUUUAAGAGAUACCAAGUGAAUU
 UAGAAGACGACGAGAGGGUAAAACUGAUUUAUJAUGCUCGGAAACGCUJGGUGAUACAAG
 AUAAAAAUAAUACAACACACCCAAAUACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
 AUCAUUUGUCAGAUUGCUU AUGGCCGUUAUGAGGGGUAUUGAUAGUCUGCGCACGUUA
 UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCGACAAUUAUGCUGCAGCAU
 AUUGUACUGGCCUGCUGCUGGCCCGCAGGCUCUCAAUAGGUUUGGCAUGGACAAGAUC
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUAG
 CCAGGUGCCUUCACCUGCUUUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA
 AGUUUUUGGUGCCCUGAAGGGAGCUGUGGAUGGAGGCUUGUCUAUCCCUCACAGUACCA
 AACGAUUCCCUGGUUAUGAUUCUGAAAGCAAGGAAUUUAUGCAGAAGUACAUCGGAAAG
 CACAUCAUGGCCAGAAUGUUGCAGAUUACAUGGCCUACUAAUGGAAGAAGAUGAAGA
 UGCUUACAAGAAACAGUUCUCUCAAUACAUAAAGAACAGCGUAACUCCAGACAUGAUGG
 AGGAGAUGUAUAAGAAAGCUCAUGCUGCUUACGAGAGAAUCCAGGUCUAUGAAAAGAAG
CCCAAGAAAGAAGUAAAAAGAAGAGGUGGAACCGUCCCAAAUGUCCCUUGCUCAGAA
 GAAGGAUGGGUAGCUAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
 AGAGCUAAACCCAGC

FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA Oligonucleotides

726-39-01	5'-GCTCAAGAACATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTG-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAACATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtgaaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggacccttatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caagggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCGGCAUAGACCCGAGCAGCCUGUCCUUCGGGAUGUGGAAAGGAGAUCC
CCGUCCCCUUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAACGAGGUCCUC
AACGGCCAGAACGCCAGUAGCCGGGAGCGUGGACCCUAUGUCUACAGGGAGUUCAGACA
AAAGGUCAACAUCAACCUCUCAAUGACAACGACACCGUGUCCUUCGUGGAGAACCGCAGC
UCCAUUUCCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUJGUACUGCCUAACA
UCUUGGUCCUGGGGGCUCGAUAIUGAUGGAGAGCAAGCCUGUGAGCCUGAAGCUGAUG
AUGACCUUGGCGCUGGUACCAUGGCCAGCGUGCUUUUAUGAACGCACAGUUGGUGA
GAUCCUGUGGGCUAUGACGAUCCUUCGUGCAUUUUCUCAACACGUACCUCCAGACAU
GCUUCCCAUAAAGGGAAAUUUGGCCUGUUUGUUGGGGAUGAACAAACUCGAAUUCUGGG
UCUUCACUGUCUUCACGGGCGUCCAGAAUUCAGCAGGAUCCAUCUGGUGGACAAUUGG
AACGGACUCAGCAAGAUCGAUUUAUUGGCAUUCAGAGCAGUGUAACAUGAUCAAUGGGAC
UUCCGGGCAGAUGUGGGACCCUUCAUGACACCCGAAUCCUCGCUGGAAUUCUUCAGCC
CGGAGGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU
CCCACGUACGCUUCACGGCCCGAUACUCUGUUUGCCACGGGUCCGUCUACCCACC
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU
UGGUGGCCUCUGUUUCUCUCCCACCCCCACUUUUAAACGGCCGACCCUGUGUUGUCAG
AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCUUGUUCUAGACAUCCAUU
CGGUACUGGGAUCCCCAUGAACGUUCUGUGAAGAUGCAGCUGAGCCCUACAUCAA
AUCUGUCAAGGGCAUCGGCAAACAGGGAAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU
GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGUUGGAGGCCUCCU
GUUGCUGGUGCCAUCAUCUGCCAACUGCGCAGCCAGGAGAAAUGCUUUUUGUUUUGGA
GUGGUAGUAAAAAGGGCUCCAGGAUAAGGAGGCCAUCAGGCCUACUCUGAGUCCUGA
UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAACCCAAGCUCUAGGGGUCCUGAAGACA
CUAUAAAGCCCCCCAAACCUGAUAGCUUGGUACAGACCAGCCACCCAGUCCUACACCCCG
CUUCUUGAGGACUCUCAGCGGACAGCCCACCAAGGCCAUGGCCUGAGCCCCAGAUGU
CACACCUGUCCGCACGCACGGCACAUGGAUGGCCACGCAUGUGCAAAAACAACUCAGGGA
CCAG

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01 5'-taatacgactcactataggacggaagtccaaagagcatcactg-3' (SEQ ID NO:286)

761-57-03 5'-gcaggtacctggtccgta-3' (SEQ ID NO:287)

781-65-01 5'-TET-ggaagtccaagagca-3' (SEQ ID NO:288)

781-65-02 5'-TET-aatggcttcttggg-3' (SEQ ID NO:289)

781-65-03 5'-TET-ggcgtcgccc-3' (SEQ ID NO:290)

781-65-04 5'-TET-tacttccgcatcgtc-3' (SEQ ID NO:291)

781-65-05 5'-TET-cttcttccctagttgtg-3' (SEQ ID NO:292)

781-65-06 5'-TET-tgcctggccgt-3' (SEQ ID NO:293)

781-65-07 5'-TET-gactctactaagaacc-3' (SEQ ID NO:294)

781-73-01 5'-TET-ccatcttagtggcgt-3' (SEQ ID NO:295)

781-73-02 5'-TET-caacaagtgcctgg-3' (SEQ ID NO:296)

781-85-01 5'-TET-aacacggcgtcac-3' (SEQ ID NO:297)

781-85-02 5'-TET-tgattaccccgagg-3' (SEQ ID NO:298)

781-85-03 5'-TET-acgctgtttcctg-3' (SEQ ID NO:299)

781-85-04 5'-TET-tgagacacacctgtacaa-3' (SEQ ID NO:300)

781-85-05 5'-TET-gacggagacagtgg-3' (SEQ ID NO:301)

781-85-06 5'-TET-caagcgagggagag-3' (SEQ ID NO:302)

FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

FIGURE 81A**Human Interleukin-1 beta (IL-1 β) Oligonucleotides**

720-82-01 5'-

gtaatttaatacgactcactatagggaaagggtgcagtttgccaaggagtgctaaag-3'

(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaaacatcat-3'

(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)

781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)

781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)

781-50-04 5'-TET-catttaccatgaaatatcc-3' (SEQ ID NO:309)

781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)

781-50-06 5'-TET-cccttagtctgctagc-3' (SEQ ID NO:311)

781-50-07 5'-TET-ttcaagtgttaacttattaacc-3' (SEQ ID NO:312)

781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)

781-72-02 5'-TET-tgcagtttgccaag-3' (SEQ ID NO:314)

FIGURE 81B

Human Interleukin-1 beta (IL-1B) (GenBank Accession # M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAUAUGAUGGCCUUAAA[CAGUGGCCAAUGAGGAUG
ACUUGUUUUUGAAGCUGAUGGCCCUAACAGAUGAAGUGCCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCU[CCGACCAC[CACUACAGCAAGGG
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUUC
CCUGCC[CACAGACCUUCCAGGAGAAUGA[CUGAGCACCUCUUUCCUCAUCUUUGAA
GAAGAACCUAUCUUCUUCGACACAUGGGAU[AACGAGGCUUAUGUGCACGAUGCACCUGU
ACGAUC[ACUGAACUGCACGCUCCGGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCU[CUCCACCUC[CA[GGGACAGGAUAUGGAGCAACAAGUGGUUC
UCCAUGGUCCUUJGUACAAGGAGAAGAAAGUAAUGACAAAAUACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUAC[CUGUCCUGCG]GUUGAAAGAUGAUAGCCCACUCUACAGCU
GGAGAGUGUAGAUCCCCAAAAUACCCAAAGAAGAAGAUGGAAAGCGAUUJGUUUCAA
CAAGAUAGAAAUCAAU[AACAAGCUGGAAUJUGAG[CUCUGCCAGUUCCCAACUGGUAC[A
UCAGCACCUCUAAGCAGAAA[CAUGCCGUCUUCUGGGAGGGACCAAAG[GCGGCCAG
GAUAAUACUGACUUC[ACCA]UGCAAUJUGUGUCUUCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAU[C]UAGGGCUGGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUCUGUJGUUACACCAAUGCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCA[UCAGCCAGGACAGUCAGCUCUCUCCUU[CA
GGGCCAAUCC[CAGCCUUUJGUUGGCCAGGCCUUCUAC[CUCUCCUACUCAUUCGU
AGCCCCGCCUGACAGAAACCACGGCCACAUUUGGUUCUAAGAAACCCUCUGUCAUUCGU
CCCACAUUCUGAU[GAGCAACCGCU]UCCCUAUUUAUUUAUUJGUUJGUUJGUUUUA
UUCAUUGGUCAAUUUAUUCAAAGGGGCAAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUAAAAGCUAUGGAAUCAAUUCAAUUJGGA[CUG]GUGUGCUCUUCUUAAAUCAGU
CCUUUAAUUAAGACUGAAAAUUAUAAAGCU[CAGAUUAAA[UAAUGGGAAUUAUUAUAA[A
UGAGCAAUAUCAUACUGGUCA

FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01 5'-TET-GCATCGTTGGGTTCTCTT (SEQ ID NO:316)
448-59-02 5'-TET-ACTTAAAGATGACCAGAGC (SEQ ID NO:317)
448-79-01 CACATTGTTCTGATCATCTG (SEQ ID NO:318)
448-79-02 CGGTAACTGACTTGAATGTC (SEQ ID NO:319)
448-79-03 TAGTAACTGGATAGTATCAC (SEQ ID NO:320)
448-79-04 GACATTCAAGTCAGTTACCG (SEQ ID NO:321)
498-20-01 AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG
(SEQ ID NO:322)

498-20-02 AATTTAATACGACTCACTATACGGTAACTGACTTGAATGTC
(SEQ ID NO:323)

498-20-03 5'-TET-CACATTGTTCTGATCATCTG (SEQ ID NO:324)
498-20-04 5'-TET-CGGTAACTGACTTGAATGTC (SEQ ID NO:325)
498-40-01 5'-
AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA
(SEQ ID NO:326)

498-40-02 5'-
AGTAATTTACGACTCACTATAGGGACGGTAACTGACTTGAATGTCCAAC
(SEQ ID NO:327)

498-84-01 5'-TET-CATTCAGATGTAGCG (SEQ ID NO:328)
498-84-02 5'-TET-GACTCATCAATCAA (SEQ ID NO:329)
498-84-03 5'-TET-GATTACAAGGCTTA (SEQ ID NO:330)

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCAUCUGAAGAUCAGCUAUAGAAGAGAAAGAUCAGUUAGUCCUU
GGACCUGAUCAGCUUGAUACAAGAACUACUGAUUCAACUUCUUUGGCUUAAUUCUC
GGAAACGAUGAAAUAUACAAGUUUAUCUUGGCUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUUACUGCAGGACCCAUAGUACAAGAAGCAGAAAACCUUAAGAAAUAU
UUAAUGCAGGGUCAUUCAGAUGUAGCGGAUAUGGAACUCUUUCUUAGGCAUUUUGAAG
AAUUGGAAAGAGGGAGAGUGACAGAAAAAAUAGCAGGCCAAAUGUCUCCUUUACUU
CAAACUUUUAAAACUUUAAGAUGACCAGAGCAUCCAAAAGAGUGUGGAGACAUCA
AGGAAGACAUGAAUGUCAAGUUUUCAAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGUCGCCAGCAGCUAAAACAGGGAAGCGAAAAGGAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCAGUAAUGGUUGUCCUGCCUACAAUAUJGAAU
UUUAAAUCUAAAUCUAAUUAUAAAUAACAUUAAAUAUAGGGAAUUAUJUUUAGAC
UCAUCAAUCAAUAAGUAUUUAUAAAAGCAACUUUUGUGUAAUGAAAAGAAUUAUCUAAU
AAUUAUAGUAUUUAUUAUAAAUCUUAUCCUGUGACUGUCUCACUUAUCCUUJGUUUU
CUGACUAAUAGGCAAGGCUAUGUGAUUACAAGGCUUUUAUCUCAGGGGCCAACUAGGCA
GCCAACCUAAGCAAGAUCCCAUGGGUUGUGUUUUACUUGAUGAUACAAUGAAC
ACUUUAAGUGAAGUGAUACUAUCCAGUUACUA

FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION # AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGGAUCUGGAAUAAAUC**AGAUUGC**
GACACUGUCAAAUUGCGGGAAGCCC~~U~~AAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAAUAGCCCUGGUUAAGUAACAAUGUJUGAAUAUGAAUCUUUU
GCGAGAUGAAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUCUUGCAGUGCUUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION # X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUUCAGAAUAGGGCCGCGGUUUUUGACCUGC
UAGUCGAUCUGGCCAGACGUACUGUGGGUGGCCAGCGCGACAUACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUUAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG
CACGGAAAGGUAUAGGGCUGGCUCUCUGAGUCGGCUUAAGGUACGUGCCGUCCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

FIGURE 83B**Earwig R2 element (SEQ ID NO:333)**

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCU[CUCAGCUG]GCUCACUUGCUGUUUAAGUG
AUAAA[ACCGUUGUUUUU]UAGU[GGGUAUUCUUUACGCUUUCGUAGGAGCGAGUCCAC
AC[UUCUUGGAGCA[AUCCGGGU[AGUGCCUAAAC[GCAUUUCUCAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAGGGUGUAGAUCAGGCCGUCUGUUUCUCCCCCGGA
GCUCGCUCCCUUGGUUCCUUUAUAUUUUAACAUCAUCAGAAACA[GACAUUAA[CAUCUA
CUGAUCCAUUU[UCGCCGGCGUACGCCACG[AUCGGAGGGUGGG[AUCUCGGGGUCUU
CCGAUCCUAAUCCAUGAUGAU[JACGA[CCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG

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